

# STIC Search Report Biotech-Chem Library

### STIC Database Tereburg

TO: Janet Epps-Ford

**Art Unit: 1653** 

Location: REM-2C05&2C18 Serial Number: 09/915543

Friday, June 10, 2005

From: Beverly Shears

**Location: Biotech-Chem Library** 

**REM 1A54** 

Phone: 571-272-2528

beverly.shears@uspto.gov

### Steated Notes

#### **Protein Sequence Searches – February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.



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STIC-Biotech/ChemLi	ib .	(99)	274			
From: Sent: To: Subject:	Epps-Ford, Janet Thursday, June 02 STIC-Biotech/Che Amino acid sequer	mLib				
Application No. 09/915,543	•					
solated polypeptides comp	risina:				,	-C.
a) a peptide consisting of a		204 of SEQ ID NO	D: 15;		25	10.
or		RN	142	-6	V.	•
o) a peptide consisting of a	umino acide 349 to 1	S84 of SEO ID NO	' ' ' ∩·15·	•	O.	
wherein said isolated polype				•	•	
Please search all pending a	ınd commercial ami	ino acid database	es.			
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\_\_\_\_ CM-1 STN Elapsed time: \_\_\_\_ Pre-S Dialog CPU time:\_\_\_\_ Type of Search \_\_\_\_ APS Total time: \_\_\_ N.A. Sequence \_\_\_\_ Geninfo Number of Searches: \_\_\_\_ A.A. Sequence \_\_ SDC Number of Databases: \_ DARC/Questel \_\_\_ Structure \_\_\_\_\_ Bibliographic Other CGN

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Database :
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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183
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PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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(without alignments)
125.671 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	υ	.Δ.	(LJ	2	_	No.	Result
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27.9		•	•	•	٠	27.9	•	•	٠	28.4	28.4	28.4	28.7	28.7	œ	9	9	29.0	9	9	9	29.8	30.1	30.1	30.1	30.6		31.1	Match	Query
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- 1	pol polyprotein -	protein E	hypothetical prote	hypothetical prote	probable alpha hel	probable alpha hel	O.	conserved hypothet	Ζ.	, pyruvate dehydroge	transcription init	probable transcrip	phytochrome В - во			mismatch DNA recog	Oi	hypothetical prote	ALR protein - huma	ALR protein - huma	5-ca	phytochrome B - ri	Rho GTPase activat	hex regulon repres		hypothetical prote	topoisomerase I-re	œ.	Description	

Yeast 11, A;Title: S a delta el

Sequence analysis

element.

A; Molecule type: DNA A; Residues: 1-584 < VAN>

A;Cross-references: UNIPROT:P53632; EMBL:Z48149; NID:g663234; PID:g663237 R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. Yeast 11, 1069-1075, 1995

of a 44 kb DNA fragment of yeast chromosome XV including the

45	44	43	42	41	40	39	38	37	36	35	34	υ S	32	31	30
49	49.5	49.5	49.5	49.5	50	50	50	50	50	50	50.5	51	51	51	51
26.8	27.0	27.0	27.0	27.0	27.3	27.3	27.3	27.3	27.3	27.3	27.6	27.9	27.9	27.9	27.9
310	2101	830	336	302	1236	1162	788	319	275	273	835	1464	1161	1161	1047
N	N	N	N	ــ	N	N	N	N	N	N	N	N	N	N	N
A84142	A42184	T18860	S72858	TPCHTC	B36329	D83454	S67595	S49771	H69843	H69337	AD2441	S58984	G81915	G81186	G90684
L-lactate dehydrog	nuclear mitotic ap	hypothetical prote	hypothetical prote	troponin T, cardia	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	endopeptidase Clp	development protei	hypothetical prote	conserved hypothet	ATP-dependent dsDN

## ALIGNMENTS

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topoisomerase I-related protein TRF4 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein HRC584; protein 00716; protein YOL115w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S51882; S59158; S58774; S66811
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
                                                                                                                                                                                                                                                                                                                             RESULT 2
S51882
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Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0551
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                                                       submitted to the EMBL Data Library, January 1995
A;Description: Sequence analysis of a 44kb DNA fragment of
and a Delta.
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C; Superfamily: sbcC protein
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A; Reference number: S51848
A; Accession: S51882
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A; Residues: 1-1034 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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transcription regulator, RpiR family Atu2598 [imported] - Agrobacterium tumefaciens (st C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AE2895 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, Cerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
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A;Cross-references: UNIPROT:Q9NT51; EMBL:AL137528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
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A;Map position: 15L
C;Keywords: nucleus
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A; Molecule type: DNA
A; Residues: 1-584 <SAD>
A; Residues: 1-584 <SAD>
A; Cross-references: EMBL: U31355; NID: g950225; PIDN: AAC49091.1;
A; Cross-references: EMBL: U31355; PIDN: A
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A;Title: Isolation of mutants of Saccharomyces cerevisiae requiring DNA topoisomerase
A;Reference number: S58774; MUID:96109595; PMID:8647385
                                                                                                                                                                                                           AE2895
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A; Accession: T46372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z48149; NID:g663234; PIDN:CAA88145.1; PID:g663237
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R;Sadoff, B.U.; Heath-Pagliuso, S.; Castano, I.B.; Zhu, Y.; Kieff, F.S.; Christman, M.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S59156; MUID:96076631; PMID:7502582 A;Accession: S59158
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A;Cross-references: EMB
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10; Mismatches
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                                                                                                                                                                                                                           C;Accession: B59436
R;Goward, M.E.; Huckle, E.J.
submitted to GenBank, April
A;Reference number: B59436
A;Accession: B59436
                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-643 < GOW
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""" ches 12; Conserve
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A; Residues: 1-295 < KUR>
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A; Residues: 1-287 < KUR>
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      30.1%;
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C;Species: Homo sapiens (man)
C;Date: 03-Jun-2002 #sequence_revision
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A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                 A;Cross-references: UNIPROT:Q9NSG0; GB:CAB90248; PID:g7711011; PIDN:CAB90248.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: circular chromosome C; Superfamily: hypothetical protein ybbH
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Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                         Rho GTPase activating protein RhoGAP8 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: circular chromosome C; Superfamily: hypothetical protein
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A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8UCA0; GB:AE007869; PIDN:AAK88321.1; PID:g15157797; GSPDB:G
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C;Species: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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40.0%;
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Pred. No.
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No.
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                     Length 643;
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ckelz, B.;
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1124
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.I
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A; Residues: 1-1171 < DEH>
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A;Title: phyB is evolutionarily conserved and constitutively
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R;Dehesh, K.; Tepperman, J.; Christensen, A.H.; Quail, P.H.
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RESULT
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A; Residues: 1-266 <GLA>
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;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
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                                                                                                               GLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQ 36
                                                                           GLAQANLVKREEIIVGGRNLEK-LKPLEAEFTGLQ
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                                                                                                                                                  Score 53.5; DB 2;
Pred. No. 19;
6; Mismatches 13;
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Pred. No. 72;
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                                                                                                                                                      13;
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Fsihi, H.
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A; Gene: ALR
A; Map position: 12
C; Superfamily: acute
C; Keywords: alternal
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A;Title: Structure and expression pattern of human ALR, A;Reference number: Z14954; MUID:97388474; PMID:9247308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALR protein - human
C;Species u-
                                                                                                                                                                                                                                                        RESULT 11
B70438
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C;Superfamily: acute lymphoblastic leukemia protein,
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03455
                                                     A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70438
                                                                                                                                                       hypothetical protein aq_1596 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B70438
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Gra
A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-227 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:014686; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: T03454
A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, A;Reference number: Z14954; MUID:97388474; PMID:9247308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                 Nature 392,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-5262 < PRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Prasad, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T03454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: acute lymphoblastic leukemia; Keywords: alternative splicing
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                                                                                                                   353-358, 1998
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17; Conserv
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17; Conserv
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Pred. No. 4.7e
4; Mismatches
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Pred. No. 5e+02;
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C;Species: Thermus aquaticus
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #cext_change 12-Jul-2004
C;Accession: S62790
R;Takamatsu, S; Kato, R; Kuramitsu, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cha A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Alauthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, G.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serox akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Togato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Feference number: A65580; MUID:98044033; PMID:9384377
A;Accession: E69957
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E69957
A; Note: the source is C; Genetics:
                                                                                                                                       Nucleic Acids Res. 24, 640-647, 1996
A;Title: Mismatch DNA recognition protein i
A;Reference number: S62790; MUID:96177563;
A;Accession: S62790
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                                                                      A; Molecule type: DNA
A; Residues: 1-818 < TAK>
                                                                                                                                                                                                                                                                                                                             mismatch DNA recognition protein mutS [validated] -
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                                                A; Cross-references: EMBL: D63810
                                                                                                               A;Status: preliminary; nucleic acid sequence not shown
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C;Superfamily: endopeptidase
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB
Pred. No. 33;
                     Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                               from an extremely thermophilic bacterium, PMID:8604304
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19;
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B70366
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A;Map position: 5
A;Introns: 22/2; 88/2; 117/3; 185/1; 221/3; 280/3; 349/2; 427/2; 532/2; 637/1
C;Superfamily: cholinesterase; cholinesterase homology
                                                                                                                                                                                                                                         A;Residues: 1-705 <WIL>
A;Residues: 1-705 <WIL>
A;Cross-references: UNIPROT:O01302; EMBL:Z81112; PIDN:CAB03272.1; GSPDB:GN00023; CESP:T0:
A;Experimental source: clone T02B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: aq 755
C;Superfamīly: Aquifex aeolicus hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Function:
A;Description: implicated in DNA mismatch repair; binds to DNA and specifically recognize atched DNA (validated, MUID:96177563)
                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, A;Reference number: Z19878
A;Accession: T24343
                                                                                                                                                                                                                                                                                                                                                                                          R;McMurray,
                                                                                                                                                                                                                                                                                                 A; Molecule type:
                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:066957; GB:AE000706; NID:g2983327; A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B70366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: The complete genome A; Reference number: A70300; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein aq 755 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B70366
                                                                                                                                                                                                        A; Gene: CESP: T02B5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T02B5.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Deckert,
                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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Matches
                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
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                                                                                          Similarity
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LSEEQVENTYSCLRKKSAQQILDAQLWLLQNSTYFLGA
                                    LSQEQLEH-----RERSLQTLRDIQRMLFPDEKEFTGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e of the hyperthermophilic bacterium MUID:98196666; PMID:9537320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52.5; D
Pred. No. 24;
7; Mismatches
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                                                                                        Score 52.5;
Pred. No. 75;
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                                                                                                            Length 705;
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, I
DNA Res. 8, 205-213, 2001
                                                                                           C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001
C;Accession: AD2541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: sequence extracted from NCBI backbone (NCBIN:118034, NCBIP:118036) C;Superfamily: transcription initiation factor sigma katF; transcription initiation C;Keywords: DNA binding; sigma factor; transcription initiation C;Keywords: DNA binding; sigma factor; transcription initiation F;103-328/Domain: transcription initiation factor sigma katF homology <KTF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 174, 7273-7282, 1992
A; Title: Identification of multiple RNA polymerase sigma
A; Reference number: A47017; MUID:93054341; PMID:1385387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable transcription initiation factor sigma SigB - Anabaena sp.
C;Species: Anabaena sp.
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: Intron positions not resolved (incomplete sequence) (;Superfamily: phytochrome; phytochrome homology C;Keywords: chromoprotein; photoreceptor; phytochromobilin F;233/Binding site: phytochromobilin (Cys) (covalent) #stat
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A; Residues: 1-332 < BRA>
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R;Brahamsha, B.; Haselkorn,
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A;Description: The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochr
                                                                                                                                                                     transcription initiation factor sigma sigB [imported] - Nostoc sp. (strain PCC 7120) C_iSpecies: Nostoc sp. PCC 7120
                                                                                                                                                                                                                        AD2541
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
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C;Species: Sorgh
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Complete
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num bicolor (sorghu
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Genomic Sequence of
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51.9%;
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35.5%;
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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  the Filamentous Nitrogen-fixing Cyanobacterium Ana
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                                                                                                                  Anabaena sp. strain PCC 7120
#text_change 09-Jul-2004
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                                             Sasamoto, :
M.; Yamada,
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                                             S.; Watanabe, A.; M.; Yasuda, M.;
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                            ;Cross-references:
  position:
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A;Cross-references: UNIPROT:Q9HTQ7;
A;Experimental source: strain PAO1
C;Genetics:
                             A; Cross-references: EMBL:U28373; NID:g849184; A; Cross-references: EMBL:U28373; NID:g849184; A; Cross-references: Exprision S288C (AB972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: sigB
A;Genome: plasmid
                                                                                                                       A; Reference number: S61159
A; Accession: S61174
                                                                                                                                                            submitted to the EMBL Data Library, June 1995 A;Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                           hypothetical protein YDR379w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D9481.4
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, W. V.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyruvate dehydrogenase
C;Species: Pseudomonae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q03065; GB:AP003602; A;Experimental source: strain PCC 7120
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A;Status: preliminary
                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                          C; Accession: S61174
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A; Residues: 1-572 <STO>
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;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004
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                     ;Geneti
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SGD:RGA2
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i0; MUID:20437337; PMID:10984043
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35.5%;
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Pred. No.
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Pred. No. 39;
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                                                           PIDN:AAB64815.1; PID:g849200; MIPS:YDR379w
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K.; Lim,
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SGD:S0002787;

MIPS:YDR379w

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RESULT 23
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C;Accession: A85901

C;Accession: A85901

C;Accession: A85901

R;Perna, N.T; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A85901
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A;Residues: 1-237 <STO>
A;Cross-references: GB:AE005174; NID:g12516965; PIDN:AAG57669.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable alpha helix protein yfhG [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli (C;Pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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C;Superfamily: uncharacterized conserved protein
  probable alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein YPO1778 [imported] - Yersinia pestis (strain C;Species: Yersinia pestis C;Species: Yersinia pestis (C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
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A; Residues: 1-102 < K
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                                                                                                                                                QEQLEHRERSLOTLRDIQRML 25
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llarity 52.4%;
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  protein [imported]
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Pred. No. 14;
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  Escherichia
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coli (strain K-12)
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K.; A
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ພິດ.≌
             hypothetical protein F516.4 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: D96834 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
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E91056
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A;Cross-references: UNIPROT:P37328; GB:BA000007; A;Experimental source: strain O157:H7, substrain C;Genetics:
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A; Residues: 1-23
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                                                                                                                                                                                                                                                                                                                                                                                                                       probable alpha helix protein [imported] - Escherichia coli (strain O157:H7, substrain RIN C;Species: Escherichia coli
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A;Note: sequence extracted from NCBI backbone (NCBIN:139878, NCBIP:139880)
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col.A.; Rose, D.J.; Mau, B.; Shao, Y.
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A; Title: The glnB region of the Escherichia coli chromosome.
A; Reference number: A49940; MUID:94042920; PMID:8226691
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Best Local (
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;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
;Accession: A49940; B65033
                                                                        Matches
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A.; Ecker, J.R.; Palm, Chung, M.K.; Conn, L.;

C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.

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Dewar,

Alonso,

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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96834
CDS protein F9L11.17 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: G86454 C;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
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A;Experimental source: clone C01B9
R;Steward, C.
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A;Introns: 20/2; 49/2; 113/1; 169/1; 260/2; 375/3;
C;Superfamily: Caenorhabditis elegans hypothetical
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A;Experimental source: clone ZK131
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A; Residues: 1-477 <WIL>
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C;Bpecies: Caenorhabditis elegans
C;Bpecies: Caenorhabditis elegans
C;Bate: 15-Oct.1999 #Bequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18801; T27746
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A; Residues: 1-329 < STO>
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Best Local
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Local Similarity 37.5%;
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816-820, 2000
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Pred. No.
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Pred. No. 51;
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    Alonso,
A;Status: preliminary
A;Molecule type: DNA
A;Residues 1-1047 <STO>
A;Cross-references: UNIPROT:Q8XEJ6; GB:AE005174; NID:g12513240;
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Accession: C26795
A;Molecule type: DNA
A;Residues: 1-899 <MOO>
A;Cross-references: UNIPROT:P03365; EMBL:M15122
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: C85535
                                                               R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
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C;Superfamily: pol polyprotein
C;Keywords: polyprotein; rever
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Nature 408, 816-820, 2000
                                                                                                                                                                                   ATP-dependent dsDNA exonuclease [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli
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C;Superfamily: Arabidopsis thaliana hypothetical protein At2g23160
                                                                                                                                       C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
C;Accession: C85535
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                                                                                                                                                                                                                                                            RESULT 29
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A; Title: Complete nucleotide sequence of a milk-transmitted
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Moore, R.; Dixon, M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                                                                                                           DGLSQEQLEHRERSLQTLRDIQRML 25
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                                                                                                                                                                                                                                                                                                                                                                                                                       27.9%;
milarity 40.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reverse transcriptase
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Pred. No. 1.5e+02
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                                                                                              J.D.; Rose,
Potamousis,
                                                                                                                                                                  09-Jul-2004
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                                                                                              D.J.; Mayhew
K.; Apodaca,
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PIDN: AAG54743.1;

GSPDB:G

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A;Residues: 1-1161 <TET>
A;Cross-references: UNIPROT:Q9K0P1; GB:AE002410; GB:AE002098; NID:g7225766; PIDN:AAF4097
A:Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 30
G90684
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                                                                                                                                                                                                                                                                                               R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Doughe ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scattato, V.; Masignani, V.; Pizza, Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuc A;Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-1047 <HAY>
A;Residues: 1-1047 <HAY>
A;Cross-references: UNIPROT:Q8XEJ6; GB:BA000007; PIDN:BAB33870.1; PID:g13359904; GSPDB:
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                  A; Accession: G81186
                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein NMB0545 [imported] - Neisseria meningitidis (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G81186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-dependent dsDNA exonuclease [imported] - Escherichia coli (strain 0157:H7, substrain
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C;Superfamily:
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Best Local S
Matches 12
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                                                                                                                                                   Gene: NMB0545
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;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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                                                                                                                              chromosome segregation protein SMCI
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48.0%;
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-EHRERSLQTLRDIQRMLFPDEKEFTGAQ 36
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                                                         6; Mismatches
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                                                                        Score 51; DB 2;
Pred. No. 2e+02;
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Pred. No. 1.8e+02;
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Pred. No. 1.8e+02
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Dougherty, B.
Pizza, M.
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endopeptidase Clp ATP-binding chain B [imported] - Nostoc sp. (E)Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                             F;1118-1153/Domain: EGF homology <EGF1>
F;614,618,624,673/Binding site: zinc (His, His, His, F;615/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1464 <FII>
A; Cross-references: UNIPROT: Q24132; EMBL: U34777; NID: g1002985; PIDN: AAC47015.1;
A; Note: the authors did not translate the codon for residue 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, Genetics 141, 271-281, 1995
A; Title: The tolkin gene is a tolloid/BMP-1 homologue that is ess A; Reference number: S58984; MUID:96042912; PMID:8536976
A; Accession: S58984
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(B81915

GB1915

hypothetical protein NMA0724 [imported] - Neisseria meningitidis (strain Z2491

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                              F;529-722/Domain: astacin homology <AST>
F;958-993/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0004885; C;Keywords: hydrolase; metalloproteinase;
                                                                                                            RESULT
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                                                                                          AD2441
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A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81915
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;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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S.; Jagels, K.; Leather,
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11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome segregation protein SMC:
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                    33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.9%;
                                                                                                                                                                                                                                                            Score 51; DB:
Pred. No. 2.6e-
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB Pred. No. 2e+0
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, S.; Moule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AL162754;
strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bentley, loule, S.;
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2e+02;
                                                                                                                                                                                                                                                                                    2.6e+02;
                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AL157959; NID:g7379424; PIDN:CAB84009
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                                                                                                                                                                                                                                                                                                      Length 1464;
                                                                                                                                                                                                                                                                                                                                                                    Tyr)
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        strain PCC 7120
09-Jul-2004
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C; Accession: H6983
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C; Brook, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cha A; Brilich, S.D.; Emmerson, P.T.; Entlan, K.D.; Exrington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69337
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A;Residues: 1-835 <KUR>
A;Cross-references: UNIPROT:Q8YM56; GB:BA000019; PIDN:BAB76783.1; PID:g17134222;
A;Experimental source: strain PCC 7120
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2441
                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein yjbH - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein AF0704 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Dace: 05-Dec.1997 #sequence_revision 05-Dec.1997 #text_change 09-Jul-2004 C;Accession: H69337
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A;Residues: 1-273 <KLE>
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Nakazaki, N.; Shimpo, ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Superfamily: endopeptidase Clp ATP-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:029554; GB:AE001056; GB:AE000782; NID:g2689379; PIDN:AAB905: Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1557
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGLSQEQLEHRERSLQTLRDIQRMLFPDE 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRLSEEELKLVRRSFEIIGDVVIIEIPDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%;
37.9%;
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38.2%;
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1.6e+02;
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, M.; Yasuda,
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hypothetical protein YDR175c - yeast (Sa
N;Alternate names: hypothetical protein
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 1
C;Accession: S49771
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A;Experimental source: strain 168
C;Genetics:
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A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69843
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-275 <KUN>
                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-788 <BLO>
A; Cross - references: UNIFROT: Q07381;
A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YDL060w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D2544
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
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A;Cross-references: SGD:S0002582
A;Map position: 4R
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R;Bloecker, H.; Brandt, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-319 <MUR>
A;Cross-references: UNIPROT:Q03976;
C;Genetics:
                                                                                                                                                                                                                                                 A; Reference number: $67587
A; Accession: $67595
                                                                                                                                                                                                                                                                                             submitted to the Protein
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                                                                                                                        Gene: SGD:TSR1; MIPS:YDL060w
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Best Local
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                                                                                 position: 4L
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                   27.3%;
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l protein YD9395.08c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
                   Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB Pred. No. 57;
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Pred. No. 67;
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                                                                                                                                                                                   EMBL: Z74108; NID: g1431062; PID: g1431063; GSPDB: GN000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: Z46727; NID: g1289283; PID: e223724; PID: g1289290
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                        1.8e+02
                                           DB 2;
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Conservative

9

Mismatches

2

Gaps

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R;Friesen, P.D.; Nissen, M.S.
Mol. Cell. Biol. 10, 3067-3077, 1990
A;Title: Gene organization and transcription of TED, a lepidopteran retrotransposon intellated number: A36329; MUID:90258898; PMID:1692964
A;Accession: B36329
Search completed: June 8, 2005, 03:23:55 Job time : 29.5625 secs
                                                                                            뭉
                                                                                                                                  8
                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-1236 <FRI
A;Cross-references: GB:M32662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 2 - cabbage looper transposon TED (fragment)
C;Species: Trichoplusia ni (cabbage looper)
C;Date: 01-Peb-1991 #sequence_revision 01-Feb-1991 #text_change 30-Sep-1993
C;Date: 01-Peb-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: D83454

C;Accession: D83454

R;Stover, C:K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: D83454
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1162 <5T0>
A;Residues: 1-1162 <5T0>
A;Cross-references: UNIPROT:Q91316; GB:AE004581; GB:AE004091; NID:g9947482; PIDN:AAG0491
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein PA1527 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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00 VQQSRIQHLEQSLERLQDRERRL 422
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                                                                                     QEHLENLERVFORLRESNFKIOMDKSEF
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milarity 39.1%;
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Pred. No. 2.7e+02;
8; Mismatches 6
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                                                                                                                                                                                                      Score 50; DB 2;
Pred. No. 2.9e+02
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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136
1 VYVFSTEMANKAAEAVLKGQVETIVSFI
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
VYVFSTEMANKAAEAVLKGQVETIVSFH
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2005, 03:09:59; Search time 21.4375 Seconds (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                      BB
                              G9707065
G9707060
D86398
F71315
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hypothetical prote
probable acetyl-Co
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glutaconate CoA-tr
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SgaT protein VCA02
probable D-2-hydro
dihydroxyacetone k
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Zn-dependent hydro
protein F17L21.2 (
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# ALIGNMENTS

RESULT 140812

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porphobilinogen synthase (EC 4.2.1.24) - Clostridium josui (fragment)
N;Alternate names: delta-aminolevulinic acid dehydratase
C;Species: Clostridium josui
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004
C;Accession: 140812
R;Fujino, E; Fujino, T.; Karita, S.; Sakka, K.; Ohmiya, K.
J. Bacteriol. 177, 5169-5175, 1995

A;Title: Cloning and sequencing of some genes responsible for porphyrin biosynthesis fro-A;Reference number: A57344; MUID:95394829; PMID:7665501 A;Accession: I40812 A;Status: preliminary; translated from GB/EMBL/DDBJ

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A;Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54487.1; CESP:Y87G2A.m
A;Experimental source: clone Y87G2A
C;Genetics:
                                                                                                                                                                                                           submitted to the EMBL Data Library, September 1999 A;Reference number: Z20371 A;Accession: T27465
                                                                                                                                                                                                                                                               hypothetical protein Y87G2A.m - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T27465 #sequence_revision 15-Oct-1999 #te: R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: hemB
C;Superfamily: porphobilinogen synthase
C;Keywords: carbon-oxygen lyase; hydro-lyase
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A;Residues: 1-205 <RES>
A;Cross-references: UNIPROT:Q59295; GB:D28503; NID:g536874; PIDN:BAA05863.1; PID:g556484
C;Genetics:
                                                                      A; Gene: CESP: Y87G2A.m
A; Introns: 74/1; 270/1
                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-634 <WIL>
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                                   Query Match
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 12;
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12; Conserv
                  Similarity
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ilarity 46.2%;
Conservative
Conservative
                40.48;
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Score 55; DB 2;
Pred. No. 4.4;
2; Mismatches 1
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Pred. No. 0.24;
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; Mismatches
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                                   Length 634;
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, C. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, B. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Status: nrel***
                             RESULT
F71315
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A; Cross-references: UNII
  probable response
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve A;Reference number: A96900; MUID:21359325; PMID:21359325, A;Accession: G97070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zn-dependent hydrolases, glyoxylase family [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: G97070
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                                                                                                                      WSFRSTNKAADRLAKGELENNVTF 204
                                                                                                                                                               FSTEMANKAAEAVLKGQVETIVSF 27
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  regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                UNIPROT: Q9FZL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%;
                                                                                                                                                                                                                                      36.0%;
                                                                                                                                                                                                             Score 49; DB Pred. No. 11; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 2;
Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                           GB:AE005172; NID:g9802520; PIDN:AAF99722.1;
  (atoC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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  syphilis
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                                                                                                                                                                                                                                                           Length 210;
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  spirochete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solvent-Producing Bacterium Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zeng, Q.; Gibson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tallon,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim,
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                                                                                                                                                             RESULT 7
C81380
C;Accession: C81380

R;ParKhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
                                                                                    probable D-2-hydroxyacid dehydrogenase Cj0373 {imported} - Campylobacter jejuni (strain }
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                           문
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82484
                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;143-365/Domain: RNA polymerase sigma factor F;53/Binding site: phosphate (Asp) (covalent) F;74/Binding site: phosphate (Asp) (covalent)
                                                                                                                                                                                                      C;Genetics:
A;Gene: VCA0246
                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9KMS4; GB:AE004364; GB:AE003853; NID:g9657630; PIDN:AAF9615; A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SgaT protein VCA0246 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001227; GB:AE000520; NID:g3322797; A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of Treponema pallidum, A;Reference number: A71250; MUID:98332770; PMID:9665876 A;Accession: F71315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, Tson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M. they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                 A; Residues: 1-586 < HEI>
                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: response regulator, NtrC type; response regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not
A;Molecule type: DNA
A;Residues: 1-458 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Species: Treponema pallidum subsp. pallidum (syphilis spirochete);Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Jun-2003;Accession: F71315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: D82484;
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Best Local (
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9
                                                                                        l Similarity
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                                             YVFSTEMANKA----
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YIFYSQVMTKAPLLLGLVTLIGYWLLRRDATTIIKGSIKTIVGF
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                                                                                           Conservative
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25.0%;
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                                                                                                           Score 49;
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24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
                                                                                        18;
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                                                                                        Gaps
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A; Rotacua: 1-311 < PAR>
A; Residues: 1-311 < PAR>
A; Cross-references: UNIPROT: Q9PIC9;
A; Cross-references: serotype 02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirz Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E84074
                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                 A; Description: The sequence A; Reference number: Z14441
                                                                                                                                                                                                                                                                                                             R;Edwards, J.; Wollam, C.; Dubbelde, C. submitted to the EMBL Data Library, August A;Description: The sequence of A. thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-330 <STO>
A;Cross-references: UNIPROT:Q9K7G4; GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07:
A;Experimental source: strain C-125
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A;Accession: C81380
                                                                                      A; Map position: 4
A; Introns: 49/3; :
A; Note: T27D20.16
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                                                                                                                                                                   A;Cross-references: UNIPROT:O81460; EMBL:AF076274; NID:g3293583; PID:g3377852
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                            A;Residues: 1-319 <EDW>
                                                                                                                                                                                                                                                                      A; Accession: T01822
                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T27D20.16 - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                            Species: Arabidopsis thaliana (mouse-ear cress);Date: 26-Feb-1999 #sequence_revision 26-Feb-1999
                                                                  ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Bacillus halodurans;Date: 01-Dec-2000 #text_change 09-Jul-2004;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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Best Local
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      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVFMNDVANKLTEEGLNIQFKKVGSF 295
                                                              Arabidopsis hypothetical protein F7N22.18
                                                                                                         151/3; 210/3; 269/2
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42.4%;
    34.6%;
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Pred. No. 19;
6; Mismatches
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      Score 47;
Pred. No.
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T27D20
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33;
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24;
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                         Length 319;
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    hypothetical protein T18H9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t/
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                                                                  T29695
                                                                                   RESULT 12
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: AD0623
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; R;Parkhill, J.; Dowd, L.; White, N. th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.
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F90179
                                                                                                                                                                                                                                                                               A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevent A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0623
                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable bacteriophage protein STY1061 [imported] - Salmonella enterica subsp.
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: pepQ
C;Superfamily: X-Pro aminopeptidase
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A; Residues: 1-352 < KUR>
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                                                                                                                                                                                              A;Cross-references: GB:AL513382; PIDN:CAD05454.1; PID:g16502215; GSPDB:GN00176
                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-662 <PAR>
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                                                                                                                                                                                                                                                                                                                                                         n, T.; Connerton, P.; Crc
S.; Moule, S.; O'Gaora,
ature 413, 848-852, 2001
                                                                                                                                                      Genetics:
Gene: STY1061
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Pred. No.
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#sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P25416; EMBL:X13525; NID:g2398; PID:g2399
A;Note: the authors translated the codon GCG for residue 327 as Thr
R;Lamb, H.K.; Hawkins, A.R.; Smith, M.; Harvey, I.J.; Brown, J.; Turner, G.; Roberts, C.
Mol. Gen. Genet. 223, 17-23, 1990
A;Title: Spatial and biological characterisation of the complete quinic acid utilisation
A;Reference number: S11944; MUID:91080861; PMID:2175387
                                                                                                                                                                                                          C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision
C;Accession: C69962
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A;Title: Molecular organisation of the quinic acid utilization (QUT)
A;Reference number: S08498; MUID:89181521; PMID:2976880
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                                                                                                                                                                                                                                                                                     branched-chain fatty-acid kinase homolog yqiU - Bacillus subtilis
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A; Residues: 1-326, 'T' < LAM>
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A; Residues: 1-330 < HAW>
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C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
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A; Residues: 1-586 < DUZ>
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Best Local S
Matches 7
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Similarity 40.7%;
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Pred. No. 7
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Pred. No.
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47;
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     S.; Galizzi, A.; Galler
Hosono, S.; Hullo, M.F.
Lapidus, A.; Lardinois,
, H.; Masuda, S.; Maueel
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  C;Accession: F72308
R;Nelson, K.E.; Clayton
Garrett, M.M.; Stewart,
                                                             hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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A;Residues: 1-461 <KUR>
A;Cross-references: UNIPROT:Q92WH4; GB:AL591985; PIDN:CAC48765.1; PID:A;Cross-references: UNIPROT:Q92WH4; GB:AL591985; PIDN:CAC48765.1; PID:A;Coss-references: UNIPROT:Q92WH4; GB:AL591985; PIDN:CAC48765.1; PID:A;Coss-references: Uniproting S.R.; Publer, A.; Abola, P.; Ampe, Pela, D.; Chain, P.; Cowie, A.; Long, S.R.W.; Dreano, S.; Federspiel, N.L.; Hyman, R.W.; Jones, T.Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; A;Athors: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; A;Title: The composite genome of the legume symbiont Sinorhizobium mel A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A0580; MUID:98044033; PMID:9384377
A;Accession: C69962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable aminotransferase protein (imported) - Sinorhizobium meliloti (strain 1021) magar
C; Species: Sinorhizobium meliloti
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C;Superfamily: butyrate kinase
                                                                                                                                                                                                                                                     A;Gene: SMb20379
                                                                                                                                                                                                                                                                                                             A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Finan, T.M.; Weidner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: P54532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-363 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004;Accession: E95887
                                                                                                                                          Query Match
Best Local :
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                                                     FSTEMANKAAEAVLKGQVETIVSF 27
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FATRMANNLEAIILEEGPETIAAF 222
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                                                                                                             Conservative
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                                                                                                                                     33.8%;
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                                                                                                                                     Score 46;
Pred. No.
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                                                                                                             Mismatches
                                                                                                                                        DB 2;
68;
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                                                                                                                                                               Length 461;
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N.A.; Fisher, R.F.;
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Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R. Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips,

R.J.;

Haft, D.H.; Hi A.; Richardson,

Hickey on, D.;

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R;Kearsey, S.E. submitted to the EMBL Data Library, April 1993 submitted to the EMBL Data Library, April 1993 A;Description: Lientification of an Saccharomyces
                                                                                                                                                                                   A;Map position: 13R C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase C;Keywords: biotin binding; ligase F;1-487/Domain: biotin carboxylase homology <BCH> F;615-687/Domain: lipoyl/biotin-binding homology <LPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-510, 'L', 512-799 < KEA>
A; Cross-references: EMBL: Z22558; NID:g:
A; Note: the published sequence extends
R; Odell, C.; Bowman, S.
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A;Cross-references: MIPS:YMR207c; SGD:S0004820
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                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 812-2123 <ODE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P32874; EMBL:Z49809; MIPS:YMR207c; NID:g854459; PIDN:CAA8992
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-833 < DED>
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A; Accession: S55089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9X087;
A:Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-1289 < ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Evidence for lateral gene transfer between Archaea A; Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 399,
A; Title: Ev:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S59441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: the published sequence extends beyond the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable acetyl-CoA carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Date: 08-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004;Accession: S55089; S41802; S59447;Dedman, K.; Brown, D.; Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Accession:
                                                                                                                                                               654/Binding site:
                                                                                                                                                                                                                                                                                                                                        Genetics:
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Best Local :
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YVFTEKVRNKYLELLRRGQV 528
                                       YVFSTEMANKAAEAVLKGQV 21
                                                                             33.8%;
ilarity 45.0%;
Conservative
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                                                                                                                                                                  biotin (Lys)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EC 6.4.1.2) HFA1 - yeast 61.01c; protein YM8325.08c;
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ktends beyond
                                                                               Score 46; DB
Pred. No. 3.4e
5; Mismatches
                                                                                                                                                               (covalent) #status predicted
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Pred. No. 2e+02;
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                                                                                                   3.4e+02;
                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerevisiae gene closely related to FAS
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                                                                                                                     Length 2123;
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                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAA88647.1; PID:g763183
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               A,Title: Structure and regulation of the Brwinia carotovora A,Reference number: S54744; MUID:95231512; PMID:7715600 A,Accession: S54744
                                                                                                                                                                                      N;Alternate names: endo-1,4-beta-glucanase C;Species: Erwinia carotanase
                                                                             C;Accession: S54744; S44996
R;Maee, A.; Heikinheimo, R.; Palva, E.T.
Mol. Gen. Genet. 247, 17-26, 1995
                                                                                                                                  A; Variety: SCC 3193
C; Date: 27-Oct-1995 #sequence_revision 03-Nov-1995
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A; Molecule type:
                                                                                                                                                                                                                                  cellulase (EC 3.2.1.4) CelV1 precursor - Erwinia
                                                                                                                                                                                                                                                    S54744
                                                                                                                                                                                                                                                                          RESULT 20
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1-504 <MAE>

DNA

carotovora

(SCC

3193)

#text\_change

09-Jul-2004

subspecies carotovora SCC319

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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change C;Accession: A99261 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 17, 3985, 1989
A;Title: Complete cDNA sequence coding for the MHC class A;Reference number: S04363; MUID:89282410; PMID:2499874
A;Accession: S04363
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S04363
                                                                                                                                                                                                                                                                                                                                               R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-256 <SYHs
A;Residues: 1-256 <SYHs
A;Residues: 1-256 <SYHs
A;Cross-references: UNIPROT:Q95572; EMBL:X14879; NID:g57154; PIDN:CAA33020.1;
A;Cross-references: UNIPROT:Q95572; EMBL:X14879; NID:g57154; PIDN:CAA33020.1;
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-256/Product: class II histocompatibility antigen, RT1-B alpha chain #stat
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C; Date: 28-Feb-1990 #sequence_revision
                                                                                                                                                                                          A;Cross-references: UNIPROT:Q97Z52; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutaconate CoA-transferase, subunit A C;Species: Sulfolobus solfataricus
                                                                                                                                                                        A;Gene:
                                                                                                                                                                                                                                        A;Residues: 1-268 <KUR>
                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                      A; Accession: A99261
                                                                                                                                                                                                                                                                                                                          A; Reference number: A99139
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Best Local
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Best Local Similarity
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Pred. No. 43;
3; Mismatches
                                                                                                    Score 45.5;
Pred. No. 45;
                                                                                                                                                                                                               GB:AE006641; NID:g13814274; PIDN:AAK41344.1;
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A;Gene: celV1
C;Function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein APE2472 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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A: Residues: 1-505 < COO>
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Mol. Gen. Genet. 241, 341-350, 1993
Mol. Gen. Genet. 241, 341-350, 1993
A;Title: Molecular analysis of the major cellulase (CelV)
A;Reference number: S39962; MUID:94067016; PMID:8246888
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S39962
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                                                                                                                                                                                                                                                                                                                A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                              DNA
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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C;Genetics:
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;Cross-references: UNIPROT:Q9Y912; DDBJ:AP000064; NID:g5105945; PIDN:BAA81488.1; PID:d:
;Cross-references: UNIPROT:Q9Y912; DDBJ:AP000064; NID:g5105945; PIDN:BAA81488.1; PID:d:
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Best Local
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Best Local
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, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamaz
Res. 6, 83-101, 1999
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                                                                                                                  Similarity
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Similarity 36.7%;
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                    VYLFSGEVWRRAVEATMIGGV 82
                                                          VYVFSTEMANKAAEAVLKGQV 21
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                                                                                                                                                                         Aeropyrum pernix hypothetical protein APE2472
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36.7%;
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Pred. No. 25;
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Yamazaki,
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hypothetical protein F6D5.1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96762
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Hothers: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, 1 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosme 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-555 < S'
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C;Superfamily: Arabidopsis hypothetical protein F7N22.18
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R;Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.;
                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005173; NID:g10092368; PIDN:AAG12776.1; GSPDB:GN00141
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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A; Residues: 1-451 <STO>
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A;Accession: B96495
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131
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                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
12; Conserv
                                                    FSTEMANKAAEAVLKGQVETIV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFSTEMANKAAEAVLKGQVETIVSF
FTTELAQKAGQVIAVDFIESVI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLSQKLA--AAEALIANQAEKITSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                        <STO>
                                                                                                                                  33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.0%;
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                                                                                                        8
                                                                                                                                  Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                            Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 451;
                                                                                                           Indels
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                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.; Tallon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O.; Alonso, Dewar, K.;
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Marziali,
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R;Hayashi, T.; Makino, K.; UHLEHLE, ..., Shiba, T.; Hattori, M.; VHARLE, T.; Kuhara, S.; Shiba, T.; Hattori, M.; VHARLE, T.; Kuhara, S.; Shiba, T.; Hattori, M.; VHARLE, T.; Kuhara, S.; Shiba, T.; Hattori, M.; VHARLE, C.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; VHARLE, C.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; VHARLE, C.; VHARLE, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species:
C;Date: 16-
C;Accession
                                                                                                                                                                                                                                                                                                                                hypothetical protein - Lactococcus lactis plasmid pMRC01
C;Species: Lactococcus lactis
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T43131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: F85710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein BCs2228 [imported] - Bscherichia coli (strain 0157:H7, C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D90907
                                                                                                                                                                                                                                     C;Accession: T43131
R;Dougherty, B.A.; Hill, C.; Weidman, J.F.; Richardson, Mol. Microbiol. 29, 1029-1038, 1998
A;Title: Sequence and analysis of the 60 kb conjugative.
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A;Experimental source: strain DPC3147
                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                              A;Reference number: Z22314
A;Accession: T43131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-50 <STO>
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A; Residues: 1-48 <HAY>
                                                      A;Residues: 1-126 <DOU>
A;Cross-references: UNIPROT:032777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
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                                                                                    1-126 <DOU>
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10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity 43.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YISSTSFANEMAEMRQQVMEGQI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVFSTEMANKAAE---AVLKGQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YISSTSFANEMAEMRQQVMEGQI 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVFSTEMANKAAE---AVLKGOV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%;
ilarity 43.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%;
43.5%;
                                                                                                                                                                                                                                  1998 of the 60 kb conjugative, bacteriocin-producing plasmid
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Pred. No. 10;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44.5; D
Pred. No. 11;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                      D.R.; Venter, J.C.; Ross,
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Д.,
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Matches
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Matches
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Best Local
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                                                             156
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                                                                IYKYETQMANPSVDVALK 173
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C;Genetics:
A;Genome: plasmid pMRC01
A;Note: ORF00060
                                                                                                                              A;Map position: REV1106050-1105094
A;Start codon: GTG
C;Superfamily: Methanococcus janna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein MJ1164 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tang, H.V.; Pring, D.R.; Muza, F.R.; Yan, B.
Curr. Genet. 29, 265-274, 1996
A;Title: Sorghum mitochondrial orf25 and a related chimeric
A;Reference number: S65767; MUID:96163056; PMID:8595673
                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-318 <BUL>
                                                                                                                                                                                                                                                                                                                      A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, A; Title: Complete genome sequence of the methanogenic archaec A; Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                       R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q35783; EMBL:U22068; NID:g733079; PIDN:AAA97555.1; A;Experimental source: strain IS1112C; coleoptile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein 265 - Sorghum mitochondrion C;Species: mitochondrion Sorghum bicolor (sorghum) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C;Accession: T1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-265 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated
                                                                                                                                                                                                                  A; Cross-references: UNIPROT: Q58564;
                                                                                                                                                                                                                                                                                                      A; Accession: C64445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T14645
                                                                                                                              ;Superfamily: Methanococcus jannaschii conserved hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: C64445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 32.4%; Similarity 37.5%; 9; Conservative
                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYVFSTEMANKAAEAVLKGQVETI
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VYVFSTEMANKAAEAVLK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.4%;
ilarity 33.3%;
Conservative
                                                               32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB
Pred. No. 74;
6; Mismatches
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                                           5.
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                                                                 Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB Pred. No. 34;
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                                                                                                                                                                                                                  GB:U67558; GB:L77117; NID:g1591786; PIDN:AAB99166.1;
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                                                                                                                                                                                                                                                                                                                                                   M.; Smith, H.O.; Woese, C
Methanococcus jannaschii
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A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;8eference number: A85001; MUID:20083488; PMID:10617198
A;Status: prelimina...
                                                                                                                                                                                                                                                                                                                                                           probable transposon protein [imported] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_chan; C;Accession: A85056 C;Accession: A85056 R;anonymous, The European Union Arabidopsis Genome Sequencing Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 32/1; 72/3; 315/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: mitochondrion; transmembrane protein
F;137-223/Domain: ADP,ATP carrier protein repeat homology <ACR>
                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-350 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, A;Reference number: Z19281 A;Accession: T20489
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R;Runswick, M.J.; Philippides, A.; Lauria, G.; Walker, J.E.
submitted to the EMBL Data Library, November 1993
A;Description: Extension of the mitochondrial transport superfamily: sequences of five
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A;Accession: T19105
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;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
;Accession: T19105; S44093; T20489
                                         Query Match
                                                                                    Superfamily: Arabidopsis hypothetical protein F7N22.18
                                                                                                                                          Gene: AT4g04430
                                                                                                                                                                            Cross-references: UNIPROT:Q9XEC1; GB:NC_001268; NID:g7267200; PIDN:CAB77911.1; GSPDB
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Best Local
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               Best Local
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8; Conservation
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               Similarity
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               32.4%;
44.0%;
               Score 44;
Pred. No.
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               DB 2;
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probable transport protein SgaT sgaT [imported] - Salmonella ent C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
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AG1051

enterica

subsp.

enterica

Be:

18-Nov-2002

RESULT

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A;Molecule type: DNA
A;Residues: 1-437 <KAW>
                                                                                                                                                                                                                                                                                                                                   awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                 5
                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9YAIO; DDBJ:AP000063; NID:g5105654; PIDN:BAA80969.1; PID:g51A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable DNA/pantothenate metabolism flavoprotein APE1959 - Aeropyrum pernix C_iSpecies: Aeropyrum pernix
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A;Cross-references: UNIPROT:Q8YF92; GB:AE008917; PIDN:AAL52811.1; PID:g17983649; GSPDB:GPA;Experimental source: strain 16M
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens)
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AH3455
                                                                                                                                                       C; Superfamily: pantothenate metabolism flavoprotein
                                                                                                                                                                           A;Gene: APE1959
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                                                                                               Query Match
Best Local :
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                                   8 MANKAAEAVLKGQVETIVSFH 28
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MLDKSGEAVLKG-----
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                                                                                                                                                                                                                                                                                                                                                                                             Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                            Conservative
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                                                                                             32.4%;
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SFH 419
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Pred. No.
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                                                                                               Score 44;
Pred. No.
                                                                                             Pred.
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                                                                    .3e+02;
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C;Species:
C;Date: 18-
C;Accession
R;Hayashi,
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R;Parkhill, J.; Dougan, G.; Jam
Connerton, P.; Cronin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P39301; GB:AB000491; GB:U00096; NID:g2367357; PIDN:AAC77150. A;Experimental source: strain K-12; substrain MG1655 R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 23, 2105-2119, 1995 Nucleic Aritle: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92. A;Reference number: S56314; MUID:95334362; PMID:7610040 A;Accession: S56418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D65230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG1051
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, A.; Rose, D.J.; Mau, B.; Shao, Y.
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C;Accession: D65230; S56418
                                                                      hypothetical protein EC85169 [imported] - Escherichia coli (strain 0157:H7,
                                                                                         A98275
                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                         A;Start codon: GTG
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A; Residues: 1-469, 'ACKKMOKNNWONSLLNKEF' <BUR>
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C;Species: Escherichia coli
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A; Residues: 1-476 < PAR>
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                    ;Species: Escherichia coli
;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
;Accession: A98275
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   Makino, K.; Ohnishi,
                                                                                                                                                                                                                                    Conservative
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Cronin, A.;
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Pred. No. 1.4e+02;
7; Mismatches
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Pred. No. 1.4e+02;
7; Mismatches 7
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Davis, P.; Davies, R.M.; Dowd,
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   Kurokawa,
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   K.; Ishii,
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, L.; White,
   Yokoyama,
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                                   A;Map position: 4
A;Introns: 175/3; 2
A;Note: F28M20.30
C;Keywords: glycosy
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A;Gene: sgaT
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A; Residues: 1-484 <HAY>
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A; Residues: 1-533 <BEV>
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glas iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Tille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference.number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                               R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, submitted to the Protein Sequence Database, November 1998 A;Reference number: Z15398
A;Accession: T05092
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                                                                                                                                               A;Cross-references: UNIPROT:Q9MU68; UNIPROT:081770; A;Experimental source: cultivar Columbia; BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                     probable 1,2-diacylglycerol 3-beta-galactosyltransferase
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(;Alternate names: protein F28M20.30

;Species: Arabidopsis thaliana (mouse-ear cress)

;Species: ^---1999 #sequence revision 23-Apr-1999
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                                         glycosyltransferase; hexosyltransferase
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Pred. No. 1.4e+02;
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Pred. No. 1
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  44;
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1.4e+02;
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RIMD 0509952
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imalanta, E.;
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                                                                                                                                                                                                                                                                                                 M.; Hoheisel,
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                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-619 <KAW>
A;Cross-references: DD5J:AP000060; NID:g5104188; PIDN:BAA80079.1; PID:g5104764
A;Experimental source: strain K1
A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C/Superfamily: zinc metalloendopeptidase, neutral protease type (elastase) C/Keywords: hydrolase; metalloproteinase; zinc F;1-25/Domain: signal sequence #status predicted <SIG>F;26-197/Domain: propeptide #status predicted <PRO>F;26-197/Product: vibriolysin #status predicted <PRO>F;197-609/Product: vibriolysin #status predicted <PRO>F;231-257,473-502/Disulfide bonds: #status predicted F;343,347,367/Binding site: zinc (His, His, Glu) #status predicted F;344,426/Active site: Glu, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Proceedings of the conservation 
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R;Cheng, J.C.; Shao, C.P.; Hor, L.I.
Gene 183, 255-257, 1996 A;Title: Cloning and nucleotide sequencing of the protease gene of Vibrio vulnificus. A;Reference number: JC5756; MUID:97149307; PMID:8996115
A;Recession: JC5756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable DNA ligase APE1094 - Aeropyrum pernix (strain K1)
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A; Residues: 197-216 < CH2>
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A;Residues: 1-609 <CHE>
A;Cross-references: UNIPROT:P96176; GB:U48780; NID:g1794193; PIDN:AAC44789.1; PID:g17941
A;Experimental source: strain YJ016
A;Accession: PC4496
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A;Residues: 1-609 <C
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                         Gene: APE1094
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        1 VYVFSTEMAN---
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                                                                                        Conservative
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                                                                                                                            Score 44; DB 2;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 2;
Pred. No. 1.8e+02;
                                                                                Mismatches
--KAAEAVLKGQVETI 24
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                                                                                                                                                           Length 619;
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Result
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Maximum DB seq
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Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 VYVFSTEMANKAAEAVLKGQVETIVSFH
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1: uniprot_sprot:*
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 GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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PRT; 1426 AA.  d) equence update) entation update) cl-9) (Legless homolog). ; Craniata; Vertebrata; ; Catarrhini; Hominidae; ; Catarrhini; Gatovsky D coation t (1;14) (q21;q32)	100.0%; Score 136; DB 2; Lengt: imilarity 100.0%; Pred. No. 4.2e-11; Conservative 0; Mismatches 0; Inde vyvpstemankaabavlkgovetivspH 28	d T., Bakkers J., Wilhelm W.; the switch between [beta functions.";  MW; 77347CP56FC4A815 CRC	PRT; 1425 AA. Created) Last sequence update) Last annotation update) Last annotation with the control of the co	Q9H6R2 Q6DKXJ5 Q96QN2 Q96QN2 Q9GG19 Q9FW7 Q9JFW7 Q9JFC9 Q8G3S3 Q9FZL1 Q96FX5 Q9EXS5 Q8G3S3 Q8G3S3 Q9FZL1 Q10FX2
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                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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DISBASE: Involved in a t(1;14)(q21;q32) chromosomal translocation DISBASE: Involved in a t(1;14)(q21;q32) chromosomal translocation found in a partient with precusor B-cell acute lymphoblastic leukemia (ALI). This translocation leaves the coding region intact, but may have pathogenic effects due to alterations in the expression level of BCL9. Several cases of translocations within the capression level of BCL9 several cases of translocations within the capression level of BCL9 have been found in B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Involved in signal transduction through the SUBUNIT: Binds to beta-catenin (CTNNB1), PYGO1 and PYC SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUB SPECIFICITY: Detected at low levels in thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: It is uncertain whether Met-1 or Met-27 is the initiator. CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 1391.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Ra Stapleton M., Sugdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rah Blakesley R. W., Touchman J.W., Green E.D., Dickeon M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kraywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Kraywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
          Query Match
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                                                                                                                SEQUENCE
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                                                                                                                                                                                                                SEQUENCE FROM N.A.

Brembeck F.H., Schwarz-Romond T.

Hammerschnidt M., Birchmeier W.;

"Essential role of BCL9-2 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q67FY0
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                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22341132; PubMed=12454917;
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic and genomic initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173
                                                                                                             Dev. 18:0-0(2004)
AY296060; AAQ6269
NCE 1474 AA; 15
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25; Conser
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AA; 1543
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          Score 102; DB Pred. No. 5.3e 7; Mismatches
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n; Craniata; Verto
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DB 2;
3.3e-06;
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Ostariophysi; Cypriniform
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                          Lewis S.
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       Annotation
                                                                                                                                                                                                                                                                                                                                                                                                         287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhong F.N., Zhong W., Zhou X., Zhu S., Myers B.W., Rubin G.M., Venter J.C.; sequence of Drosophila melanogaster.";
of the Drosophila melanogaster
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   euchromatic genome: a
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Bc191 protein. Name=Bc191;

musculus

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RESULT Q641L9
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Best Local
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Stapleton M., Caribon
George R.A., Guarin H., Kronman.
George R.A., Celniker S.E.;
Rubin G.M., Celniker S.E.;
"A Drosophila full length cDNA resource.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJNE-2246066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein |
George R.A., Guarin H., Kronmiller B.,
                                                                                                                                                                                                                                                                                                                    MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005634; C:nucleus; IDA. GO; GO:0030528; F:transcription GO; GO:0030177; P:positive regul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF457205; AAL91368.1; -. FlyBase; FBgn0039907; lgs.
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                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE003844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  P:segment
                                                                                                                                                                                                                                                                                                                                                                                                                                             F:transcription regulator activity; IPI.
P:positive regulation of Wnt receptor signali. . .; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF59345.2; -.
AAK93075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ig S., Basler K.;
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                                                                                                                                                                                                                                                                                                                      1169
514
534
                                                                                                                                                                                                                                                                                                                                                             1449
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                                                                                                                                                                                                                                   72.1%;
57.1%;
                                                                                                                                                                                                                                                                                         537
                                                                                                                                                                                                                                                                             153759
                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires BCL9/legless-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                  polarity determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signal transduction and PYGO.
                                                                                                                                                                                                                                                                            MW;
                                         Last
Last
                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                   Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                              Asn-rich.
Gln-rich.
Poly-Asn.
                                                                                                                                                                                                                                                                                phenotype.
I->K: In allele lgs-17P.
                                                                                                                                                                                                                                                                                                                    G->E: In allele
L->F: In allele
                                                                                                                                                                                                                                                                                                                                                                                        ARM-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                        Mismatches
                                         sequence update)
annotation update)
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                                                                                                                                                                                                                                                                            5672E01B7200ED08 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOI=10.1016/S0092-8674(02)00679-7;
                                                                                                1457
                                                                                                                                                                 1 350
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, Pacleb J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                   Segmentation polarity
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                                                                                                                                                                                                                                                                                                                      segment
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ω.,
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                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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238

VYVFTTHLANTAAEAVLQGRAESILAYH

265

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RESULT Q67FY2
ID Q6
AC Q6
DT 25
DT 25
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DT 25
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C DR BC
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RC STRAIN-C57BL/6; TISSUE-Brain;

RC STRAIN-C57BL/6; TISSUE-Brain;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RX Strausberg R.L., Feingold B.A., Grouse L.H., Schamen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Scheetz T.E.,

RA Hopkins R.F., Jordan H., Roshaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan K.J., Rubin G.M., Hong L.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Pan Jones S. J., Marra M.A.;
                                                                    Query Match
Best Local (
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Best Local (
                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                       Q67FY2;
Q67FY2;
25-OCT-2004
25-OCT-2004
25-OCT-2004
                                                                                                                                    STRAIN-C57BL/6;
Brembeck F.H., Schwarz-Romond T., Bakkers J.,
Hammerschmidt M., Birchmeier W.;
"Essential role of BCL9-2 in the switch betwee
adhesive and transcriptional functions.";
Genes Dev. 18:0-0(2004).
EMBL; AY296058; AAQ62696.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6; TISSUE=Brain;
Director MGC Project;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082304; AAH82304.1;
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         BCL9-2
                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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Mammalia; Eutheria;
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                                                  l Similarity
17; Conserv
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VYVFSTEMANKAABAVLKGQVETIVSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYVFTTHLANTAAEAVLQGRAESILAYH
                                                                                                                      1494
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                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                         (Mouse)
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                                                                                                                   AAQ62696.1; -.
AA; 156679 MW;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.1%;
60.7%;
                                                                  69.1%;
60.7%;
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28,
                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94; DB 2;
Pred. No. 8.2e-05;
                                                                    Score 94; DB 2;
Pred. No. 8.4e-05
                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                   31A9904C5923581C CRC64;
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                                                                                   Length 1494;
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                                                    Indels
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RESULT 10
Q86UU0
ID Q86UU
AC Q86UU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DE DLNB1
GN Name=
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Q617B5
ID 17B6
PAC Q6
DT 055
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Best Local (
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Best Local
Q86UU0; PRELIMINARY;
Q86UU0; O1-JUN-2003 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
DLUB11 protein.
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Genes Dev. 18:0-0(2004).

EMHI. NYACCE
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05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brembeck F.H., Schwarz-Romond T.,
Hammerschmidt M., Birchmeier W.;
"Essential role of BCL9-2 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q67FY1;
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Yasui T., Nakano T., Ohwada S., Omori Adachi S., Jigami T., Yasui T., Nakamura T., Akiyama T.; Sugano S., Ohkawara B., Shibuya H., Nakamura T., Akiyama T.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL9-2.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=B9L;
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17; Conserv
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1494 AA; 156570 MW;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Human)
                                                                                                                                                                                                                                                                                                                                                                                                AAQ62697.1;
AA; 156528
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                                                                                                                                                                                                                                                                                                                                 66.9%;
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                                      24,
24,
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                                                                                                                                                                                                                                                                                                                                                                                                MW.
                                      Last sequence update)
Last annotation update)
                                                                             Created)
                                                                                                                                                                                                                                                                                                              Score 91; DB
Pred. No. 0.00
9; Mismatches
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Last annotation updat
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                2D591F45FF3AEE36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bakkers J.,
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Best Local
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Best Local
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Q59295;
01-NOV-1997
SEQUENCE FROM N.A.
STRAIN=FERM P-9684;
MEDLINE=95394829; PubMed=7665501;
Fujino E., Fujino T., Karita S., &
"Cloning and sequencing of one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes Dev.
EMBL; AY296
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toyoda A., Hattori M., Sakaki Y., Nakagawara A., Ohki M. Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AB094091; BAC76045.1; -
                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation updat
Delta-aminolevulinic acid dehydratase (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brembeck F.H., Schwarz-Romond T., Bakkers J., Wi
Hammerschmidt M., Birchmeier W.;
"Essential role of BCL9-2 in the switch between
adhesive and transcriptional functions.";
Genes Dev. 18:0-0(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q67FY3
Q67FY3;
                                                                                                                                                                                                                                                                                                                                                                CLOJO
                                                                                                                                                                 Bacteria; Firmicutes;
                                                                                                                                                                                  Clostridium josui.
                                                                                                                                                                                                        Name=hemB
                                                                                                                                                                                                                        synthase) (ALAD)
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25-OCT-2004
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             195
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NCE 1530 AA; 159872
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nilarity 57.1%;
Conservative
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AA; 157129 MW;
                                                                                                                                                                                                                           (ALADH)
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        Karita S., Sakka K., Ohmiya
ng of some genes responsible
                                                                                                                                                               Clostridia;
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28,
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Pred. No. 0.00
7; Mismatches
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Last annotation update)
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Pred. No. 0.00
9; Mismatches
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Catarrhini; Hominidae;
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(EC 4.2.1.24)
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                                                                                                                                                                 Clostridiaceae,
          for;
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                                                                                                                                                                                                                                           (Porphobilinogen
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          porphyrin
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                    Q9U1Q4;
Q9U1Q4;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyase; Po
DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Y87G2A.5.
Name=vrs-2; ORFNames=Y87G2A.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0144; DALDHYDRTASE.

ProDom; PD002304; AlaD dehydratase; 1
PROSITE; PS00169; D ALA DEHYDRATASE;
Lyase; Porphyrin blosynthesis; Zinc.
DOMAIN 114 132 Zinc-bin
        WormBase, WBGene00006936, vrs-2.
Wormbep; Y87GA.5; CE24685.
GO; GO:0005524; F:ARP binding; IEA.
GO; GO:0004832; F:valine-tRNA ligase activity
GO; GO:0006438; P:valy1-tRNA aminoacylation;
GO; GO:0006438; P:valy1-tRNA aminoacylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentifies requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H(2)O.
-!- COFACTOR: Zinc (By similarity)
-!- PATHWAY: Siroheme biosynthesis
-!- SUBUNIT: Homooctamer (By simil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis from the anaerobic bacterium Clostridium josui.";
J. Bacteriol. 177:5169-5175(1995).
-!- CATALYTIC ACTIVITY: 2 5-aminolevulinate = porphobilinogen
                                                                                                                                                                           "Genome sequence of the nematode investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; I40812; I40812.
HSSP; P15002; 1L6S.
InterPro; IPR001731; AlaD_dehydratase.
Pfam; PF00490; ALAD; 1.
                                                                                EMBL; AL110500; CAE
HSSP; P96142; 1IVS.
                                                                                                           Submitted (MAY-1999) to
                                                                                                                         White S.;
                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                  STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D28503; BAA05863.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the ALADH family.
                                                                                                                                                                                                                     HOLLE?
                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
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  IPR002300;
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205 I
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                              CAB60428.1;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc-binding (By similarity).
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              activity; Is
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                                                                                                                                                                                                                                                                                                                    Rhabditida; Rhabditoidea;
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                                                                                                                                                                                                        platform
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Best Local (
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InterPro; IPR002303; tRNA-synt val.
InterPro; IPR0020080; tRNAsyn1 la_bind.
InterPro; IPR009080; tRNA binding arm.
InterPro; IPR009008; valRs_ IlerS_edit.
Pfam; PF00133; tRNA-synt 1; 1.
PRINTS; PR00986; TRNASYNTHVAL.
TIGRFAMS; TIGR00422; valS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002110; ANK.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR0024112; tRNA-synt_la.
InterPro; IPR002303; tRNA-synt_val.
InterPro; IPR002303; tRNA-synt_la bind.
InterPro; IPR009008; ValRS_ITERS_edit.
Pfam; PF00113; tRNA-synt_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q767M3;
Q767M3;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
980H30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB113355; BAD08425.1; -.
EMBL; AB113354; BAD08423.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004832; F:valine-tRNA ligase activity; IE
GO; GO:0006438; P:valyl-tRNA aminoacylation; IEA.
                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR00422; valS; 1.

PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.

SEQUENCE 1062 AA; 118287 MW; 619F2
                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01415; ANKYRIN.
PRINTS; PR00986; TRNASYNTHVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shigenari A., Ando A.,
Yasue H., Inoko H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-larg white,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical | Name=KIAA1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenetics 55:695-705(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clusters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequencing analysis of the swine 433-kb
located between the non-classical and classical SIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
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                                                                                                                                                                                                                               Local
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                                                                                                              FVRCQEMGEQAAKAVVSGALELSPSFH
                                                                                                                                                       YVFSTEMANKAAEAVLKGQVETIVSFH 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
1_protein KIAA1885.
PRELIMINARY;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and large white;
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                                                                                                                                                                                                     Score 55; DB 2
Pred. No. 40;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB Pred. No. 40; 2; Mismatches
PRT;
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                                                                                                                                                                                                                                                                                                  619F230CC078EEC7 CRC64;
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193
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40;
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class I gene
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Sus.
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Q72X37
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Best Local
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Best Local
            Q72X37
Q72X37,
Q72X37,
Q5_JUL_2004 (Trem)
05_JUL_2004 (Trem)
05_JUL_2004 (Trem)
Sensor histidine)
                                                                                                                                                                                                                                                                                                                                                                                                                       Q63019;
Q63019;
25-OCT-2004
25-OCT-2004
25-OCT-2004
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seque
05-JUL-2004 (TrEMBLrel. 27, Last annot
Sensor histidine kinase, putative (EC
OrderedLocusNames=BCE5541;
                                                                                                                                                                                                                                                              "Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       Brettin T.S., Bruce D., Challacombe Hitchcock P., Jackson P., Keim P., I Richardson P., Rubin E., Tice H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brettin T.S., Bruce D., Challacombe J.F., Giln Hitchcock P., Jackson P., Keim P., Longmire J. Richardson P., Rubin E., Tice H.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ EMBL; AE017225; AAT57552.1; -. GO; GO:0005524; F:ATP binding; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update
                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                          Kinase; Transferase.
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Pfam; PF02518; HATPase_C; 1.
SEQUENCE 193 AA; 21865 MW; DE1F60ACD9C3E0D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Two-component sensor protein, OrderedLocusNames=BAS5264;
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=288681;
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                                                                                              17
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12; Conserv
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                                                                                                                                                       VFSTEMANKAAEAVLKGQVETI 24
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                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                          Bacillales;
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                                                                                                                                                                                                                                                                                                                                                                                                          28, Created)
28, Last sequence update)
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(EC 2.7.3.-).
Score 54; DB Pred. No. 28; Pred. No. 28;
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Pred. No. 9
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Longmire J.,
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28;
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Lucas S.
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Best Local S
Matches 12
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Best Local S
Matches 12
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                            Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Bacillus thuringiensis Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databa EMBL; AE017355; AARG61192.1; -- GO; GO:0005524; F:ATP binding; IEA.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003594; GAF.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brettin T.S., Bruce D., Challacom
Hitchcock P., Jackson P., Keim P.
Richardson P., Rubin E., Tice H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; NCBI_TaxID=180856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=BT9727 5092;
Bacillus thuringiensis (subsp. konkukian).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                             Pfam; PF01590; GAF; 2.
Pfam; PF02518; HATPase_c; 1.
SMART; SM00065; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=97-27;
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Pfam; PF02518; HATPase_c; 1.
SMART; SM00065; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6HAM4
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InterPro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=14960714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI TaxID=222523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349
   349
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523 AA; 59731 N
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LFSLTFMTKGAEAVLKGQNEKV 370
                                                                 VFSTEMANKAAEAVLKGQVETI 24
                                                                                                                                                                                                                                                                            523
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                            59795 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.7%;
54.5%;
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                                                                                                                                                               39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Challacombe J.F., Gilna., Keim P., Longmire J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase.
MW; 4F105468CA527ABF CRC64;
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Pred. No.
                                                                                                                                  Score 54; DB Pred. No. 28; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                        2C87843AEA3C3AA7 CRC64;
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                                                                                                                                                                                                   Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P., Han C., Hill I
Lucas S., Okinaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Hill K.,
                                                                                                                                  0,
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RESULT 19
Q71SH3
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Best Local S
Matches 11
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                                                                         PubMed=12447439; DOI=10.1038/nature01183;

Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,

Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,

Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,

Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,

Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,

Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,

Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,

Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,

Lian L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
OSJNBa0008M17.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aminotransferase family.

EMBL, AF297651; AAQ14479.1; -
GO; GO:0030170; F:pyridoxal phosphate binding;
GO; GO:00008483; F:transaminase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPRO05814; Aminotrans_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).

Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00202; Aminotran_3; 1. —
Aminotransferase; Pyridoxal phosphate; Transferase.
SEQUENCE 516 AA; 56474 MW; DCC7AC57563C403B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q71SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Senescent
Ansari M.I., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
                             Gramene;
                                                   EMBL; AL662950
HSSP; P16932;
                                                                                                                                                                                                           Lan L., Lai
Han B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
PubMed=12447439; [
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7XN11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Senescent leaf;
TISSUE-Senescent leaf;
Ansari M.I., Lee R.H., Chen S.C.G.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-|- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative aminotransferase.
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  GO:0030170;
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                             Q7XN11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                1DKA.
  F:pyridoxal phosphate binding;
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Pred. No. 38;
4; Mismatches
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Last annotation updat
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                                                                                                                                 class-III
                                                                                                                                                                                  chromosome
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                                                                                                                               pyridoxal-phosphate-dependent
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        IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 516;
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RESULT RESULT ID RESULT RESULT 22
Q6MG21
ID Q6MG2
AC Q6MG2
DT 05-JU
DT 0
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RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RA Go; Go:0005524; FlATP binding; IEA.
GO; GO:000524; FlATP binding; IEA.
GO; GO:0006439; P:valyl-tRNA aminoacylation; IEA.
GO; GO:0006439; P:valyl-tRNA aminoacylation; IEA.
GO; GO:0006439; P:valyl-tRNA aminoacylation; IEA.
GO; GO:000439; CRNA-synt I.
DR InterPro; IPR002309; tRNA-synt I.
DR InterPro; IPR00309; tRNA-synt Val.
GO; GO:000539; TRNA-synt I.
DR InterPro; IPR00309; tRNA-synt I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 12
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Best Local :
                                    Q6MG21
Q6MG21;
Q5MG21;
Q5-JUL-2004 (TrEMB:
Q5-JUL-2004 (TrEMB:
Q5-JUL-2004 (TrEMB:
Q5-JUL-2004 (TrEMB:
MIAA1885 protein.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus cDNA fis, clone TRACH3031400, weakly similar to Valyl-
tRNA synthetase 2 (EC 6.1.1.9).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0422; vals; 1.
PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
    Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aminoacyl-tRNA synthetase SEQUENCE 1059 AA; 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00133; tRNA-synt_1; 1. PRINTS; PR00986; TRNASYNTHVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481
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    norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVRCQEMGDRAAKAVESGALELWPSFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FATRLANNLEELILKEGPETIAAF
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                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.2%;
llarity 44.4%;
Conservative
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                                                                                                                                                                                                                                                                        PRELIMINARY;
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45.8%;
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27,
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Last annotation updat
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Pred. No. 1.1e
5; Mismatches
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                                                                                                                                                                                                                                                                            PRT;
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; Murinae; Mus.
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RESULT
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ID Z79
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TISSUB-Embryonic intestinal tract;
Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
Nagase T., Ohara O., Koga H.;
"Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
CDNAs Identified by Screening of Terminal Sequences of cDNA Clones
Randomly Sampled from Size-Fractionated Libraries.";
DNA Res. 11:205-218(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q69Z78
Q69Z78; PRELIMINARY;
Q69Z78; 25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: UUUDBAD; ERNA-SYNT 1a.
InterPro; IPR002300; ERNA-SYNT 1a.
InterPro; IPR002103; ERNA-SYNT val.
InterPro; IPR002303; ERNA-SYNT 1a bind.
InterPro; IPR009080; ERNASYN 1a bind.
InterPro; IPR009080; ValRS_ILERS_edit.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ c
EMBL; BX883047; CAE84026.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000524; F:valine-tRNA ligase activity;
GO; GO:0004832; F:vally-tRNA aminoacylation; IE
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKIAA1885 protein (Fragment).
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Sudbrak R., Reinhardt
Submitted (DEC-2003) t
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PubMed=15060004; DOI=10.1101/gr.1987704;
Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.
Hurt P., Walter L., Guenther E., Reinhardt R., Himmelbauer H.;
Inoko H., Lehrach H., Guenther E. Reinhardt R., Himmelbauer H.;
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=mKIAA1885
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PROSITE; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Brown Norway;
Boehm S., Borzym K.,
Lang N., Lehrack S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genomic sequence and comparative histocompatibility complex."; Genome Res. 14:631-639(2004).
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PRINTS; PR00986; TRNASYNTHVAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVRCQEMGDRAAKAVESGALELWPSFH 507
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.2%;
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93 MW; 4BF57C6962DA50CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Created)
, Last sequence up
, Last annotation
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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GO; GO:0004832; F:valine-tRNA ligase activity;
GO; GO:0006438; P:valyl-tRNA minoacylation; IE
InterPro; IPR002300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt T.
InterPro; IPR001412; tRNA-synt T.
InterPro; IPR002303; tRNA-synt val.
InterPro; IPR002303; tRNA-synt val.
FRINTS; PR00133; tRNA-synt 1; I.
PRINTS; PR00386; TRNASYNTHVAL.
  Q84P52
Q84P52;
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01-JUN-2003 (TrEMBLro
01-MAR-2004 (TrEMBLro
Gamma-aminobutyrate t
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838 (2001).
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Q97JA0;
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PROSITE; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=CAC1386;
Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Zn-dependent hydrolasse, glyoxylase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 824 / DSM 792 / VKM B-
MEDLINE=21359325; PubMed=11466286;
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Pfam; PF00753; Lactamase_B; 1.
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12; Conserv
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243 AA; 26880 MW;
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PS00178; AA_TRNA_LIGASE_I;
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(TrEMBLrel. 24, Created)
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(TrEMBLrel. 26, Last annotation update)
outyrate transaminase subunit isozyme 3 (EC
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Pred. No. 35;
ll; Mismatches
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                            Length 243;
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    2.6.1.19).
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RESULT 26
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Best Local Similarity
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Best Local
                                                                                                                                 FlyBase; FBgn0027079; Aats-val.
GO; GO:0005524; F:ATF binding; IEA.
GO; GO:0004832; F:Valine-tRNA ligase activity; IEA.
GO; GO:0004838; P:Valy1-tRNA aminoacylation; IEA.
InterPro; IPR002300; tRNA-synt_1a.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR003303; tRNA-synt_1.
InterPro; IPR003033; tRNA-synt_1.
InterPro; IPR009080; tRNA-synt_1a_bind.
InterPro; IPR01978; tRNA-binding_arm.
InterPro; IPR01978; tRNA-binding_arm.
InterPro; IPR01978; tRNA-binding_arm.
InterPro; IPR01978; tRNA-synt_1; 1.
PRINTS; PR0033; tRNA-synt_1; 1.
PRINTS; PR00986; TRNASYNTHVAL.
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01-DEC-2001
01-DEC-2001
01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wayu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hachycera;

Neoptera; Endopterygota; Diptera; Brachycera;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003867; F:4-aminobutyrate transaminase GO; GO:0030170; F:pyridoxal phosphate binding; GO; GO:0016740; F:transferase activity; IEA.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster

lamiids; Solanales; Solanaceae; Solanum.
                                                                     SEQUENCE
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FlyBase; FBgn00270
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                                                                                         ; TIGR00422;
PS00178; AA
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                                                                   AA_TRNA_LIGASE_I; 1.
A; 118331 MW; 56F322C7414EEAC4 CRC64;
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45.8%;
37.5%;
40.7%;
                                                                                                                  valS;
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19,
26,
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the class-III pyric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB Pred. No. 77; 3; Mismatches
Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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DB 2; 1
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pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insecta; Pterygoera; Muscomorpha;
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                        Length 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Matches

Conservative

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RESULT 27

QPV611

ID QPV61

AC QPV61

DT QPV61

DT QPV61

DT QPV61

DT QPV61

GN NCB1

RN NCB1

RN NCB1

RN SEQ1

RA Amay

RA Amay

RA Bal

RA RA Ch

RA Gal

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                  Science [2]
                              Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9V6L1;
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Name=Aats-val; ORFNames=CG4062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                  MEDLINE=22426065; PubMed=12537568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006;
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                                                                                                                                                                                                                                                                                                                                    FROM N.A.
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           euchromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10731132; DOI=10.1126/science.287.5461.2185; ker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
       genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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SYV_FURN
ID SYV F
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DT 01-FE
DT 25-OC
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OC Fugu
OC Actin
OC Actin
OC Tetra
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Best Local :
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Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertlebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
25-OCT-2004 (Rel. 45, Last annotation
Valyl-trnA synthetase (EC 6.1.1.9) (Va
                                                                                               Name=VARS1;
                                                                                                                                                                                       P49696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002300; tRNA-synt_1a.
InterPro; IPR002141; tRNA-synt_7a.
InterPro; IPR002303; tRNA-synt_val.
InterPro; IPR002000; tRNA-synt_bind.
InterPro; IPR009080; tRNA-synt_ding_arm.
InterPro; IPR009008; valx8_Ilers_edit.
Pfam; PF00133; tRNA-synt_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S. Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.I Smith C.D., Tupy J.L., Whitfied R.J., Bayraktaroglu L., Berman B Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0027079; Aats-val.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004832; F:valine-tRNA ligase activity;
GO; GO:0006438; P:valyl-tRNA aminoacylation; IF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGR004;
PROSITE; PS00178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashburner M., Celniker S.E.; "The transposable elements of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patel S., Frise E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426070; PubMed=12537573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaminker J.S., Bergman
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P96142; 1IVS
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                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1049
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΑA;
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                                                                                                                                                                                                                                                                                                                                                                                             37.5%;
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53 MW; 13A513ABF69E8EEB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 51;
Pred. No.
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                             (Valine--tRNA ligase)
                                                                                                                                                                                                            1217
                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1049;
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                                                                                                                (ValRS).
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RESULT 29
Q89JQ
ID Q89JQ
AC Q89JQ
DT 01-JU
DT 01-MA
DT 01-MA
DT 01-MA
DE Blr52
GN Order
OC Brady
OX NCB1
RN [1]
RP SEQUI
RC STRAI
RA KANEDLI
RA Sagar
RA KOADAI
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Best Local S
Matches 10
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InterPro; IPRO10446; GST_Cterm.
InterPro; IPRO024046; GST_Cterm.
InterPro; IPRO02300; tRNA-synt_la.
InterPro; IPRO01412; tRNA-synt_val.
InterPro; IPRO10978; tRNA-synt_val.
InterPro; IPRO10978; tRNA-syn_la_bind.
InterPro; IPRO109080; tRNA-syn_la_bind.
InterPro; IPRO09080; ValRS_IERS_edit.
Pfam; PF00043; GST_C; 1.
PRINTS; PRO09086; TRNA-SYNT_1; 1.
PRINTS; PRO09086; TRNA-SYNT_1; 1.
PRINTS; PRO09086; TRNA-SYNT_1; 1.
                                                                                                                                                                    Q89JQ9 PRELIMINARY;
Q89JQ9;
01-JUN-2003 (TrEMBLrel. 24, C
01-JUN-2003 (TrEMBLrel. 24, L
01-MAR-2004 (TrEMBLrel. 26, L
Blr5213 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lim E.H., Corrochano L.M., Elgar G., Brenner S.;
"Genomic structure and sequence analysis of the valyl-tRNA synthetase
gene of the Japanese pufferfish, Fugu rubripes.";
DNA Seq. 7:141-151(1997).
-I- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
+ L-valyl-tRNA(Val).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uch
Sasamoto S., Watenabe A., Idesawa K., Iriguchi M.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wa
                                                                     SEQUENCE FROM N.A.
                                                                                                                Bradyrhizobiaceae;
                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                         OrderedLocusNames=blr5213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aminoacyl-tRNA synthetase; ATP-binding; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X91856; CAA62967.1; -. HSSP; P96142; 1IVS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=31033;
                                                                                                NCBI_TaxID=375;
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                                                                                                                                                                                                                                                                                                                626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                               YVSCSDMGKQAADAVREGRLKIIPDHH
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809
812
1217
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813
812
                                                                                                                Bradyrhizobium.
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                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Pred. No. 1.8e
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "KMSKS" region
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                                                                                                                                                                                                                                            PRT;
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5E08AF24B5C8A7A1
                                                                                                                                                                                                                                                                                                                652
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J. 1.8e+02;
9;
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                             Uchiumi T
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 Wada T., Yamada
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RESULT 31
Q814L6
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AC Q814L
DT 01-JU
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Best Local S
Matches 10
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Best Local S
Matches 13
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GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005910; F:DNA ligase (ATP) activity; IE

GO; GO:0006310; P:DNA recombination; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO:GO:0006281; P:DNA repair; IEA.

GO:GO:0006281; D:DNA ligase.

Fiam; PF04679; DNA ligase.

Pfam; PF04679; DNA ligase.
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082521;
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NCBI TaxID=80170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete
SEQUENCE
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DNA Res: 9:189-197(2002).
EMBL; ADORGERA TO 12002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aluru M., Curry J., O'Connell M.;
"Nucleotide Sequence of a Probable Aminotransferase
No. AF085149) from Habanero Chile. (PGR98-182).";
Plant Physiol. 118:1102-1102(1998).
-i- SIMILARITY: Belongs to the class-III pyridoxal-p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
Aminotransferase; Pyridoxal phosphate; Transferase.
SEQUENCE 459 AA; 50729 MW; 02ABB4D728B524E4 CRC64;
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GO; GO:0030170; F:pyridoxal phosphate binding;
GO; GO:0008483; F:transaminase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.8%;
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48.1%;
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Pred. No. 70;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB Pred. No. 95; 4; Mismatches
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Q814L6; Q814L6; 01-JUN-2003 01-JUN-2003

(TrEMBLrel. (TrEMBLrel. PRELIMINARY;

24, 24,

Last sequence update)

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RESULT
Q9H6R2
ID Q9
AC Q9
DT 011
DT 0
                                                                                                            EMBL; AK02551,

HSSP, P96142; 1ITS.

GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006526; F:Valline-tRNA ligase activity; IEA.
GO; GO:0006438; P:Valline-tRNA aminoacylation; IEA.

GO; GO:0006438; P:Valy1-tRNA aminoacylation; IEA.

InterPro; IPR002300; tRNA-synt_la.

R InterPro; IPR002300; tRNA-synt_val.

R InterPro; IPR009300; tRNA-synt_la bind.

JR InterPro; IPR009008; ValRS_IIERS_edit.

JR Pfam; PF00133; tRNA-synt_l; 1.

PFam; PF00133; tRNA-synt_l; 1.

OR Pfam; PF00133; TRNASYNTHVAL.

OR PTNNTS; PR00986; TRNASYNTHVAL.
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Best Local (
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Q9H6R2;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sh Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AK025218; BAB15191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein FLJ21965.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete
SEQUENCE
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SMART; SM00387; HATPase C; 1.
Complete proteome; Transferase.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003018; GAF.
Pfam; PF01590; GAF; 2.
Pfam; PF01590; GAF; 2.
Pfam; PF02518; HATPase C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Bacillus cereus Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Overbeek R., Kyrpides N.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=226900;
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Bacteria: Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=BC5412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2004 (TrEMBLrel.
Two-component sensor pro
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       l Similarity
12; Conserv
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(TrEMBLrel. 16, Last sequence up
(TrEMBLrel. 26, Last annotation
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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50.0%;
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                                      36.8%;
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Score 50; DB 2; 1
Pred. No. 1.3e+02;
4; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                          C9E37EE1D742B7F1 CRC64;
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annotation update)
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                                                                         Length 642;
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       Indels
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Shibahara
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   <u>,</u>
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RESULT 33
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA RA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                  Matches
                                                                               Query Match
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25-OCT-2004
25-OCT-2004
                                                                                                                                                                                 EMBL; BC073838; AAH73838.1; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006483; F:valine-tRNA ligase activity; IE.

GO; GO:0006438; P:valyl-tRNA aminoacylation; IEA.

InterPro; IPR002300; tRNA-synt_la.

InterPro; IPR002303; tRNA-synt_val.

InterPro; IPR002303; tRNA-synt_val.

InterPro; IPR0020303; tRNA-synt_la.

InterPro; IPR009080; tRNA-synt_la.

InterPro; IPR009080; tRNA-synt_la.

Pfam; PF00133; tRNA-synt_l.

InterPro; IPR009018; ValRS IleRS_edit.
                                                                                                                                                                                                                                                                                                                                Director MGC Project;
Submitted (JUN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                              Pfam; PF00133; tRNA-synt 1; 1.
PRINTS; PR00986; TRNASYNTHVAL.
                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=VARS2L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARS2L protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-0CT-2004
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75
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                               N
                                                                 12;
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                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
FVRCQEMGARAAKAVESGALELSPSFH
                               YVFSTEMANKAAEAVLKGQVETIVSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVRCQEMGARAAKAVESGALELSPSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVFSTEMANKAAEAVLKGQVETIVSFH
                                                                                                                                   657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                  ₽,
                                                                                                                                  73196 MW;
                                                                               36.8%;
                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28,
                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                             Score 50; DB 2;
Pred. No. 1.4e+02
4; Mismatches 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                  BC34A3735FFA400A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
101
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                                                                                                Length 657
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1 J.E.,
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RESULT 34 Q96GN2

A U

Q96GN2;

PRELIMINARY;

733

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RESULT
Q96Q02
ID QS
AC QS
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DT HG
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RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer R.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer R.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer R.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
RA Alnes S.J. Marra M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                    Q96Q02 PRELIMINARY;
Q96Q02;
01-DEC-2001 (TrEMBLrel. 19, 0
01-DEC-2001 (TrEMBLrel. 19, 1
01-MAR-2004 (TrEMBLrel. 26, 1
KIAA1885 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'ARsz.;
Name=VARS2L;
Homo sapiens (Human).
Homo sapiens (Human).
Horia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002110; ANK.
InterPro; IPR002300; tRNA-synt la.
InterPro; IPR002303; tRNA-synt val.
InterPro; IPR002008; tRNA-synt la bind.
InterPro; IPR009008; Valks Ileks edit.
InterPro; IPR009008; Valks Ileks edit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009355; AAH09355.2; -. HSSP; P96142; IIVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARS2L protein (Fragment)
Name=VARS2L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                             KIAA1885 protein
Name=KIAA1885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00133; tRNA-synt_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005524; F:ATP binding; IEA.
GO:0004832; F:valine-tRNA ligase activity;
GO:0006438; P:valyl-tRNA aminoacylation; II
sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR01415; ANKYRIN.
PR00986; TRNASYNTHVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                          FVRCQEMGARAAKAVESGALELSPSFH 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.8%;
nilarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81230 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 50; DB;
; Pred. No. 1.5e.
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last seq
Last ann
                                                                                    Last sequence up
Last annotation
                                                                                                                                                  Created)
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                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B0433DC47AAB6721 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence update)
annotation update)
                                                                                                                     sequence update)
                                                                                                                                                                                                                    1098
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                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 37
Q9LFW7
ID Q9LFW
AC Q9LFW
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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 12
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_val.
InterPro; IPR002303; tRNA-synt_val.
InterPro; IPR002303; tRNAsyn_la_bind.
InterPro; IPR009008; tRNAsyn_la_bind.
InterPro; IPR009008; valrs_Iers_edit.
Pfam; PF00133; tRNA-synt_l; l.
PRINTS; PR00906; TRNASYNTHVAL.
TIGRFAMs; TIGR00422; valS; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8GGI9;
Q8GGI9;
01-MAR-2003
01-MAR-2003
01-MAR-2004
Q9LFW7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 8:179-187(2001).
EMBL; AB067472; BAB67778.1;
HSSP; P96142; 1IVS.
Genew; HGNC:21642; VARS2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bringel F., Hubert J.-C.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF514870; AAO15990.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo NCBI_TaxID=9606; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CCM3626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=abc1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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GO; GO:0004832; F:valine-tRNA ligase activity; II
GO; GO:0006438; P:valyl-tRNA aminoacylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactobacillus plantarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The complete sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Prediction of the coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Kikuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           large proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TaxID=1590;
                                                                                                                                                                                                       176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516
                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                       VYSTDLLAKAAE---KGQVDAI
                                                                                                                                                                                                                                                                   VFSTEMANKAAEAVLKGQVETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVRCQEMGARAAKAVESGALELSPSFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1098 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 26,
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Pred. No. 2.3e+02;
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STRAIN-JCM 10545 / 7;
MEDLINE=21456156; PubMed=11572479;
MEDLINE=21456156; PubMed=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Kawarabayasi Y., Hino Y., Horikawa H., Hosoyama A., Fukui S.,
Sekine M., Haba S.-I., Bankai A., Kosugi H., Hosoyama A., Fukui S.,
Sekine M., Haba S.-I., Ankai A., Nakazawa H., Takamiya M., Kato Y.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Yoshizawa T., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
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Q976C9;
01-DEC-2001
01-DEC-2001
01-JUN-2003
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
Hypothetical protein ST0252.
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Khan S., Brooks S., Buehler B., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukhazeky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus tokodaii.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update
Hypoxanthine-guanine phosphoribosyltransferase.
Name=hprT; OrderedLocusNames=BL1681;
Bifidobacterium longum.
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Bifidobacteri
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PROSITE; PS00103; PUR_PXR_PR_TRANSFER; 1.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 187 AA; 20617 MW; E697C3C127277DB1 CRC6
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EMBL; AE014802; AAN25468.1; -.

HSSP; O33799; 1J7J.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:000422; F:hypoxanthine phosphoribosyltransferase

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0009116; P:nucleoside metabolism; IEA.

GO; GO:0006166; P:purine ribonucleoside salvage; IEA.
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Pessi G., Zwahlen M.-C., Desiere
Pridmore R.D., Arigoni F.;
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DNA Res. 8:123-140(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of Bifidobacterium longum reflects to the human gastrointestinal tract."; Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
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Bifidobacteriaceae; Bifido
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4; Mismatches
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Pred. No.
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3; Mismatches
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Search completed: June Job time: 136.25 secs
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RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Theologie A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologie A., Ecker J.;
RI Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RRI SUBMBL; ACC004557; AAF99722.1; -.
RMBL; ACC004557; DeSaysb.
RGO; GO:0005634; C:nucleus; IEA.
RGO; GO:0005634; C:nucleus; IEA.
RGO; GO:0006355; F:carbon utilization; IEA.
RGO; GO:0006355; F:carbon utilization; IEA.
RGO; GO:0006355; F:carbon utilization; DNA-dependent; IEA.
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                               GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004089; F:carbonate dehydratase activity;
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0015976; P:carbon utilization; IEA.
GO; GO:0015976; P:carbon utilization; DA.
GO; GO:006355; P:regulation of transcription, DNA
InterPro; IPR001382; PAH.
InterPro; IPR001382; PAH.
InterPro; IPR001765; Prok pint Coanhd.
Pfam; PF02671; PAH; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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181 WSFRSTNKAADRLAKGELENNVTF 204
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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5 mus musculu
                                                                            bacillus an
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agrobacteri
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saccharomyc
methanopyru
homo sapien
homo sapien
drosophila
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                         homo sapien
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45	44	43	42	41	40	39	38	37	36	35	34	u u	32
53.5	53.5	53.5	53.5	54	54	54	54.5	54.5	54.5	55	55	55	55
29.2	29.2	29.2	29.2	29.5	29.5	29.5	29.8	29.8	29.8	30.1	30.1	30.1	30.1
974	266	208	155	832	554	326	1171	1171	174	718	464	433	428
N	N	N	N	N	N	N	N	Н	Н	۲	N	N	N
Q73CF5	Q8Y9X2	Q6PZ60	Q8VD56	Q64WV9	Q7R1P0	Q6D1R6	Q84LN8	PHYB_ORYSA	ASC3 MOUSE	RHG8 HUMAN	Q86XV6	Q8IZM6	Q6PJW1
Q73cf5 bacillus ce	Q8y9x2 listeria mo	Q6pz60 mycobacteri	Q8vd56 rattus norv				Q84ln8 oryza sativ				homo	Q8izm6 homo sapien	homo

## ALIGNMENTS

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This SWISS-PROT e between the Swist the European Biois use by non-prof modified and this entities requires	-!- CAUTION: -!- CAUTION: frameshif	intact, be expression the 3' un	-!- DISEASE: Involve found in a patie leukemia (ALL).	-!- TISSUE SP	-!- SUBCELLUL	pygopus to th Cell 109:47-6	Murone M., Zu	FUNCTION. MEDLINE=21952490;	gene (BCL9) a Blood 91:1873	Dyer M.J.S.; "Molecular cl	Willis T.G., Zalcberg Jadayel D.M., Bastard	SEQUENCE FROM N.A. TISSUE=Fetal brain;	NCBI_TaxID=9606;	Eukaryota; Metazoa; Mammalia; Eutheria;	Name=BCL9;		28-FEB-2003 ( 28-FEB-2003 (	IT 1 HUMAN BCL9 HUMAN 000512;
This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as immodified and this statement is not removed. Use entities requires a license agreement (See http.)	CAUTION: It is uncertain whether Met-1 or Met-27 is CAUTION: Ref.1 sequence differs from that shown due frameshift in position 1391.	, but may have pathogen sion level of BCL9. Sev untranslated region of ancies.	Involved in a tapatient with partient with partient with parties. This transfer is the control of the control o	ECIFICITY: Detection of the second se	SUBUNIT: Binds to beta-catenin (CTNNB1), SUBCELLULAR LOCATION: Nuclear (Probable)	wnc/wingless signating requires ocus/regress meanaced pygopus to the nuclear beta-catenin-TCF complex."; Cell 109:47-60(2002).	M., Zuellig S., Basler K.;	490; PubMed=1195	(BCL9) at chromosome 1q21." 1 91:1873-1881(1998).	Dyer M.J.S.; "Molecular cloning of translocation t(1;14)(q21;q32) def	Willis T.G., Zalcberg I.R., Coignet Jadayel D.M., Bastard C., Treleaven	N.A. brain;		tazoa; Chordata; heria: Primates:		l. 44, Last 9 protein	(Rel. 41, Created) (Rel. 41, Last seg	STANDARD;
yright. It is post of Bioinformat Institute. The trions as long is not removed. agreement (See	in whether Met-1 e differs from to 1391.	nogenic effects . Several cases on of BCL9 have	(1;14) (q21;q32 precusor B-cel nslocation lea	cted at low le intestine, and	gnai transduct atenin (CTNNB1 clear (Probabl	catenin-TCF co	K., Nellen U. K.;	55446; DOI=10.	21.";	ocation t(1;14	net L. ven J.			; Craniata; Vertebrata; : Catarrhini; Hominidae		annotation update (Bcl-9) (Legless h	i) equence update	PRT; 1426 A
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lified and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/	l or Met-27 is the initiator. That shown due to a	e been found in B-cell	DISEASE: Involved in a t(1;14) (g21;g32) chromosomal translocation found in a patient with precusor B-cell acute lymphoblastic leukemia (ALL). This translocation leaves the coding region	TISSUE SPECIFICITY: Detected at low levels in thymus, prostate, testis, ovary and small intestine, and at lower levels in spleen,	FUNCTION: INVOLVED IN BIGHAL CIANBOUCCION CINCURGI CHE MIL PALLMAY. SUBUNIT: Binds to beta-catenin (CTNNBI), PYGO1 and PYGO2. SUBCELIULAR LOCATION: Nuclear (Probable).	recture	, Chacterjee s	2-8674 (02) 00679		) (q21;q32) defines a novel	J.A., Wlodarska I., Stul M., G., Catovsky D., Silva M.L.M.,			ertebrata; Euteleostomi; Hominidae; Homo.		(Legless homolog).	<u>ٽ</u>	AA.

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RESULT 3
Q6NRE2
ID Q6NR
AC Q6NR
DT 05-J
DT 05-J
DT 05-J
DT MGC8
GN Name
OS Xeno
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Best Local S
Matches 36
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q67FX9
Q67FX9;
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                    Q6NRE2;
                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adhesive and transcriptional functions."; Genes Dev. 18:0-0(2004).
                                                                                                                                                                                                          05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brembeck F.H., Schwarz-Romond T. Hammerschmidt M., Birchmeier W., "Essential role of BCL9-2 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                       SEQUENCE FROM N.A.
                                                                                                                                                                    Name=MGC83888;
                                                                                                                                                                                 MGC83888 protein.
                                                                                                                                                                                                                                                   05-JUL-2004
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DOMAIN
  TISSUE=Oocytes;
                                                           NCBI_TaxID=8355;
                                                                                   Xenopodinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:1008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 28, (TrEMBLrel. 28, 4 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
                                                                                                                                                                                                  (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translocation;
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llarity 100.0%;
Conservative 0
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AA; 148970
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Pred. No. 5.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 183; Db 1;
Pred. No. 2.7e-14;
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CTNNB1-binding
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RESULT 4
Q67FYO
ID Q67F
AC Q67F
AC Q67F
DT 25-O
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DT 25-O
DT Bcl9
OS Bracc
OC Euka
OC Acti
OC CYppx
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DR EMBLI
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Klausmer R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Hopkins R.F., Jordan H., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Wollano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Knzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.I. Mayra M.A.
Best Loc
Matches
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25-OCT-2004
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25-OCT-2004
                                                                 EMBL; AY2
SEQUENCE
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
                                                                                                  Genes
                                                                                                                                  SEQUENCE FROM N.A.

Brembeck F.H., Schwarz-Romond T.

Hammerschnidt M., Birchmeier W.;

"Essential role of BCL9-2 in the
                                                                                                                                                                                                                                                                                        Brachydanio
                                                                                                                                                                                                                                                                                                           Bc19
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC070813; AAH70813.1; -.
                                                                                                                adhesive and transcriptional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones S.J., Marra M.A.; "Generation and initial analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                     NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                Dev. 18:0-0(2004
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NCE 796 AA;
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Conservative
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                                                                                                                                                                  Schwarz-Romond T.,
                                                                 AAQ62698.
AA; 1543
            90.3%;
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Pred. No.
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1.1e-09;
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5e-12;
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                                         X PubMed=12477932; DOI=10.1073/pnas.242603899;
X PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
X Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Altschul S.F., Jordan H., Moore T., Wax S.I., Wang J., Hong L.,
X Altschul S.F., Jordan H., Moore T., Wax S.I., Wang J., Hong L.,
X Altschul S.F., Jordan H., Moore T., Wax S.I., Wang J., Hong L.,
X Altschul S.F., Loquellan K., Farmer A.A., Rubin G.M., Hong L.,
X Altschul S.F., Loquellano N.A., Becers G.J., Abramson R.D., Mullahy S.J.,
X Altscharde S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
X Altscharde S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
X Altscharde S., Worley K.C., Sodergren B.J., Lu X., Gibbs R.A.,
X Altscharde S., Morley D.M., Sodergren B.J., Lu X., Gibbs R.A.,
X Altschul S., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
X Willalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Whiting M., Touchman J.W., Green B.D., Dickson M.C.,
X Halkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
X Alther S. J., Marra M. A.,
X Alther S. J., Marra M. A.,
X Alther S. J., Marra M. A.,
X Alther S. J., Warra M. A.,
X Alther S. J
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Best Local S
Matches 22
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Q641L9;
25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; Cyprinidae; Danio.
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Bc19-2.
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22; Conser
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Pred. No. 2.4e-05;
3; Mismatches 0
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                                                      Butterfield Y.S., A., Schein J.E.,
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Q67FY2;
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Brembeck F.H., Schwarz-Romond T., Bakkers J., Wi
Hammerschmidt M., Birchmeier W.;

"Essential role of BCL9-2 in the switch between
adhesive and transcriptional functions.";
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Genes Dev. 18:0-0(2004).
EMBL; AY296058; AAQ62696.1;
SEQUENCE 1494 AA; 156679
                                                                               Brembeck F.H., Schwarz-Romond
Hammerschmidt M., Birchmeier
"Essential role of BCL9-2 in
adhesive and transcriptional
                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6;
Brembeck F.H., Schwarz-Romond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes Dev. 18:0-0(2004).
EMBL; AY296059; AAQ62697.1; -.
SEQUENCE 1494 AA; 156528 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6; TISSUE-Brain; Director MGC Project; Submitted (SEP-2004) to the E
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                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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Rodentia;
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the switch
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Pred. No. 7.3e-05;
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Pred. No. 7.5e-05;
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RESULT 11
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Adachi S., Jigami T., Yasui T., N.
Adachi S., Ohkawara B., Shibuya H
Submitted (DEC-2003) to the EMBL/
EMBL; AB128033; BAD24964.1; -.
SEQUENCE 1494 AA; 156570 MW;
                                                                                                                                                                                                                                                                                  Toyoda A., Hattori M., Sakaki Y., Nakagawara & Submitted (CCT-2002) to the EMBL/GenBank/DDBJ SEQUENCE 1400 **
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BCL9 DROME
Q961D9; Q9V4D2;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Kubo T., Arai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                        STANDARD;
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                                                                                                                                                                                                                     Score 109; DB 2;
Pred. No. 7.6e-05
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Pred. No. 7.5e-05;
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Catarrhini; Hominidae;
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                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                   Mismatches
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H., Nakamura
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d. No. 7.
                                                                                                                                                                                                                                                                                    8415C2EDB7AA9C0C CRC64;
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agawara A., Ohki M.,
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    RX MEDLINGE 2019606, PubMed=10731132; DOI=10.1126/Science.287.5461.2185; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., A Stuton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA MARINE, Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Adril J.E., Agbayani A., An H.-J., Addrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Berkova D., Botchan M.R., Bouck J., Brokstein P., Belshakov S., Ra Beson K.Y., Benos P.V., Berman B.P., Brandara I., Bolshakov S., Barder J., Buller H., Gadieu E., Center A., Chandra I., Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P., Ra Burtis K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra I., Cherty J.M., Cavley S., Dahlke C., Davenport L.B., Davies P., Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foeler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Rodiev C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Poeler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Harris M.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Ra Hostin D., Houston K.A., Novin K., Wei M.-H. Deywam C., Lai Z., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Hostin D., Houston K.A., Nixon K., Nusskern D.R., Pacleb J.M., Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Shue B.C., Stapleton M., Strong R., Sun B., 
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28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Bcl-9 homolog (Legless protein).

Name=1gs; Synonyms=BCL9; ORFNames=CG2041;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insect Neoptera; Endopterygota; Diptera; Brachycera; Mu Ephydroidea; Drosophilidae; Drosophila.
                Stapleton M., Carlson J.W
George R.A., Guarin H., K
Rubin G.M., Celniker S.E.
                                                                      STRAIN=Berkeley; TISSUB=Embryo;
MEDLINE=22426066; PubMed=12537569;
                                                                                                                                                                                                                                    MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.I
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                               "Annotation of the Drosophila melanogaster euchromatic
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                                                                                                                                                           Biol.
                                                                                                                                                                              review.
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full-length
                                                          Carlson J.W., Brokstein
                                       Kronmiller
  cDNA resource.";
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era; Muscomorpha;
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bJ.M.,
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RESULT 12
Q77LIG
Q77LIG
AC Q7RLIG
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DT 01-MA
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DT 01-MA
DT 01-MA
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CT 01-MA
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Best Local
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Q7RLG2;
Q1-MAR-2004
01-MAR-2004
STRAIN=17XNL;
STRAIN=17XNL;
STRAIN=12368865; DOI=10.1038/nature01099;
PubMed=12368865; DOI=10.1038/nature01099;
Carlcon J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Carlcon J.M., Angiuoli S.V., Shlen J.E., Selengut J.D., Koo H.! Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.! Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L. Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities
or send a
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EMBL; AY(
EMBL; AF4
FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Wnt/wingless signaling requires BCL9/legless-mediated pygopus to the nuclear beta-catenin-TCF complex."; Cell 109:47-60(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     520
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AY051651; AAK93075.1; -.
AF457205; AAL91368.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F:transcription regulator activity; IPI.
P:positive regulation of Wnt receptor signali. . .; IPI.
P:segment polarity determination; IMP.
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G->E: In allele !
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22;
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RESULT 13
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                                                                                                                                                                                                                              Pfam; PF00488; Muts_V; 1.
Pfam; PF01713; Smr; 1.
ProDom; PD001263; MutS_C; 1
SMART; SM00534; MUTSac; 1.
SMART; SM00533; MUTSd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q89YQ1
Q89YQ1;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                 Complete
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=VPI-5482 / ATCC 29148;
MEDLINB=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000432; MutS C.
InterPro; IPR007696; MutS III.
InterPro; IPR002655; Smr/MutS2_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 299:2074-2076(2003).
-!- SIMILARITY: Belongs to the DNA mismatch
EMBL; AE016946; AA079785.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA mismatch repair prote
OrderedLocusNames=BT4680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 192 AA; 22971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence and comparative analysis parasite Plasmodium yoelli yoelii."; Nature 419:512-519 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003684; F:damaged DNA binding;
GO; GO:0006259; P:DNA metabolism; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=818;
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; AABL01000710; EAA22049.1; -.
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87
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                                            w
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                                                                                                                                                                                                        proteome; DNA-binding.
                                            LSQEQUEHRERSLQTLRDIQRMLFPDEKE
LDEQELFDLRRSLETIRDIVRFLHRNEEE
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44.8%;
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Pred. No. 7.4;
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                                                                                                                                                                                    3B40B0168D6E7076 CRC64;
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AC Q7VNS5;

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RA MUNSON
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RA INTERPRODER;
DR INTERPRODER;
KW Complet
SQ SEQUENC
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Best Local
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Q8Z8Y6;
Q1-MAR-2002
EMBL; AL627266; CADORBSO.1; -.
GO; GO:0016302; C:membrane; IEA.
GO; GO:0005634; F:C:mucleus; IEA.
GO; GO:0005524; F:AITP binding; IEA.
GO; GO:0005524; F:AITPase activity, coupled to transmembrane
GO; GO:00042626; F:AITPase activity; IEA.
GO; GO:0004527; F:exonuclease activity; IEA.
GO; GO:00070559; P:chromosome segregation; IEA.
GO; GO:0006259; P:DNA metabolism; IEA.
GO; GO:0006259; P:DNA metabolism; IEA.
GO; GO:000618; SmCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia I Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Chill M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., With Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Chill M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., With Larsen T.S., Laster S., Moule S., O'Gaora P., Parry C., Chill M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., With Larsen T.S., Laster S., Moule S., O'Gaora P., Parry C., Chill M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., With Larsen T.S., Laster S., Moule S., O'Gaora P., Parry C., Chilling M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., With Larsen T.S., Laster S., Moule S., O'Gaora P., Parry C., Chilling M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., With Larsen T.S., Laster S., Moule S., O'Gaora P., Parry C., Chilling M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., With Larsen T.S., Laster B., Manney M., Skelton J., Stevens K., With Larsen T.S., Laster B., Manney M., Skelton J., Stevens K., With Larsen T.S., Laster B., Manney M., Skelton J., Stevens K., With Larsen T.S., Laster B., Manney M., Skelton J., Stevens K., With Larsen T.S., Manney M., Skelton J., Stevens K., With Larsen T.S., Manney M., Skelton J., Skelto
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Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur Johnson L., Nguyen D., Wang J., Forst C., Hood L.;

"The complete genome sequence of Haemophilus ducreyi.";

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases

EMBL; AE017152; AAP95377 1;

InterPro; IPR008314; UCP029143.

ProDom; PD030073; UCP029143; 1.
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Name=sbcC; OrderedLocusNames=STY0429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whitehead S., Barrell B.G.;
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Pasteurellaceae; Haemophilus.
NCBI_TaxID=730;
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OrderedLocusNames=HD0412;
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01-OCT-2003
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J. Bacteriu.

J. Bacteriu.

J. Bacteriu.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0005634; C:nucleus; IEA.

JR GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004527; F:exonuclease activity, Coupled DR GO; GO:0004527; F:exonuclease activity; IEA.

GO; GO:0004527; F:exonuclease activity; IEA.

GO; GO:0007059; P:chromosome segregation; GO; GO:0006259; P:DNA metabolism; IEA.

DR GO; GO:0006810; P:transport; IEA.

ThterPro; IPR003439; ABC transporter.

TDR004592; SbcC.

TDR004592; SbcC.
Q8ZRE
Q8ZRE3
ID Q8ZRE
AC Q8ZRE
DT 01-MA
DT 01-MA
DT 01-OC
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Q83SZ9;
01-JUN-2003
                                                                Q8ZRE3;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-CCT-2003 (TrEMBLrel. 25, Last anno
ATP-dependent daDNA exonuclease.
Name=sbcC; OrderedLocusNames=STM0395;
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SEQUENCE
                                                                                                                                                                                                            Q8ZRE3
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SEQUENCE
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STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner
"Comparative genomics of Salmonella enterica serova
and CT18.";
                                                Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=sbcC; OrderedLocusNames=t2469; Salmonella typhi.
                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02463; SMC_N; TIGRFAMs; TIGRO0618; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
Enterobacteriaceae; Salmon
    Enterobacteriaceae;
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1034 AA; 116759 MW;
                                                                                                                                                                                                                                                                                                                          LADEQLQQLEASLQALTDEEKRLLADQQ 240
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0; C:membrane; IEA.
4; C:nucleus; IEA.
4; F:AIP binding; IEA.
6; F:AIFase activity, coupled
6; F:Exonuclease activity; IEA.
9; P:Chromosome segregation; I
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                     Gammaproteobacteria; Enterobacteriales;
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                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB Pred. No. 2.1e 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     6
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Pred. No. 2.1e
6; Mismatches
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RESULT
Q7Q3P6
                                                                                                                                                                            SOUTH THE STATE OF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        á
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                                                                                      Query Match
Best Local S
Matches 14
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7Q3P6;
Q7Q3P6;
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Ano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
EMBL; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leonard S., Nguyen C., Sco
Ryan E., Sun H., Florea L.
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21534948, PubMed=11677609; DOI=10.108/35101614; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre McClelland M., Sanderson K.E., Spieth J., Clifton S.W., L. Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., L Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvan Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston B. Wilcon B. T., Miller W., Stoneking T., Whan M.,
                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02463; SMC N; 1.
TIGRAMS; TIGRO0618; SbCc; 1.
Complete proteome; Exonuclease.
SEQUENCE 1046 AA; 117823 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgCP10924 (Fragment).
Name=agCG50252; ORFNames=ENSANGG00000009382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                          InterPro; IPR009060; UBA like.
InterPro; IPR001012; UBX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L; AE008713; AAL19349.1; -.
GO:0016020; C:membrane; IEA.
GO:0005634; C:nucleus; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0004526; F:ATPase activity, coupled to transmembrane (GO:004527; F:exonuclease activity; IEA.
GO:0007059; P:chromosome segregation; IEA.
GO:0006259; P:DNA metabolism; IEA.
GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213
                                                                                                                                                                                                                                                                                    reliminary data.
AAAB01008964; EAA12408.1;
  408
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                                                                                                          Similarity
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                                                                                                                                                                                                                   PS50033; UBX;
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RIERRFRSTDTMRDIYHFIFCHPDAPDSFEIT
                                         QLEHRERSLOTLRDIQRMLF----
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                                                                                        Conservative
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                                                                                                                                                                            54397 MW;
                                                                                                          30.9%;
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Last
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                                                                                   Score 56.5; DB 2;
Pred. No. 1e+02;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB
Pred. No. 2.1e
6; Mismatches
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                                                                                                                                                                            5A7EC8C1E8C30576 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nematocera; Culicoidea; Anopheles
                                            PDEKEFT
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                                                                                                                               Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                                                                                                                                                                     which
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                                                                                   Gaps
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RESULT 19
TRF4_YEAST
ID TRF4_YEAST
                                                 Query Match
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01-OCT-1996
                                              Mitosis.
SEQUENCE
                                                                                                                                                                   EMBL; AY723865; AAU09782.1; ...
PIR; S51882; S51882.
Germonline; 143537; -.
SGD; S000005475; TRF4.
GG; GG:0005534; C:nucleus; IDA.
GG; GG:0003887; F:DNA-directed DNA polymerase activity; IDA.
GG; GG:0000387; F:DNA topological change; IGI.
GG; GG:0007076; P:mtrclic chromosome condensation; IMP.
InterPro; IPR0012301; PAP_25A_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as modified and this statement is not removed. Usentitles requires a license agreement (See htt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=TRF4; OrderedLocusNames=YOL115W; ORFNames=00716, HRC584; Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetacese; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
25-CCT-2004 (Rel. 45, Last annotation
Topoisomerase 1-related protein TRF4.
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U31355; AAC49091.1; -.
EMBL; Z48149; CAA88145.1; -.
EMBL; Z74857; CAA99134.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system."; Submitted (AUG-2004) to the EMBL/GenBank/DDB databases.
-!- FUNCTION: Essential protein required for proper nuclear division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Tay
Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.
Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camary
Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in mitosis. May mediate mitotic chromosome condens-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE-96076631; PubMed=7502582;
Vandenbol M., Durand P., Portetelle D., Hilger F.;
Vandenbol M., Durand P., Hilger F.;
Vandenbol M., Directory M., Hilger F.;
Vandenbol M., Portetelle D., Hilger F.;
Vandenbol M., Portetelle D., Hilger F.;
Vandenbol M., Directory M., Hilger F.;
Vandenbol M., Durand P., Portetelle D., Hilger F.;
Vandenbol M., Durand P., Durand P., Portetelle D., Hilger F.;
Vandenbol M., Durand P., Durand P., Durand P., Portetelle D., Hilger F.;
Vandenbol M., Durand P., Durand P., Durand P., Portetelle D., Hiller M., Portetelle D., Hiller
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Sadoff B.U., Heatl
                                                                                                  Pfam;
                                                                                                                         Pfam; PF01909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              suppressor gene for tRNA-Gly, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation of mutants of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Christman M.F.;
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                                                                                                                                                   InterPro;
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                                                                                                  PF03828;
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                                                                                                                         IPR002058; PAP_assoc.
1909; NTP_transf_2; 1.
                                                   584
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                                                                                             PAP_assoc;
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                                                 66030 MW; 8A58B29E4BFDC022 CRC64;
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  Score
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  56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 moved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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  Length 584;
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RESULT OF SECOND SOLUTION OF SECOND OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                            Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
                                                                                                                                                                                                                             Q9NT51;
Q9NT51;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=AV19 / DSM 6324 / JCM 9639;

STRAIN=AV19 / DSM 6324 / JCM 9639;

MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Natale D.A., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

EMBL; AE010374; AAM02048.1; -.

CO. GO.0005524; F.ATP binding; IEA.
                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein DKFZp434P1818 (Fragment).
Name=DKFZp434P1818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8TGZ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM0049
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0000166; F:nuclectide binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotati
Archaea-specific Superfamily II helicase.
     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=MK0835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003593; AAA ATPase.
InterPro; IPR001410; DEAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00382; AAA; 1.
SM00487; DEXDc; 1.
SM00490; HELICc; 1.
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                 GFSQTLLEKLERLLHELRDIDRVVEMVDPAFDPAE 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       818 AA;
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                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome; Helicase; Hydrolase.
18 AA; 91715 MW; C2136200A710817E CRC64;
                                                                           Primates;
                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.6%;
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10; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 2; Le
Pred. No. 2.1e+02;
4; Mismatches 16;
                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Q9VXU1
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Q9Y2H2
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                                                                      Q9VXU1;
Q9VXU1;
01-MAY-2000
01-OCT-2002
01-MAR-2004
                       CG33206-PB.
ORFNames=CG33206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:17054; INPP5F.
InterPro; IPR002013; Syja.]
Pfam; PF02383; Syja.N; 1.
PROSITE; PS50275; SAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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Drosophila melanogaster
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Pfam; PF02383; Syja N; 1.
PROSITE; PS50275; SAC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99246063; PubMed=10231032;
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                                                                                                                                                                                                                                                                                                      ENORSHOELISQLLOSYMKLLLPDDEKFHG
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                                                                                             (TrEMBLrel.
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                                                                      13,
22,
26,
(Fruit fly)
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Pred. No.
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The German cDNA Consortium;
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Pred. No. 2.3e
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.1e+02;
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update)
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Han K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
RA Harli J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaseley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek R., Gong F., Gornell J.H., Gu Z., Gabart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegvam C.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Liang Y., Lin X.,
RA Merkulov G., Wilshina N.V., Mobarry C., Morris J., Moshredi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Shupski M.P., Smith T.,
RA Melson D.R., Walshing A.C., Stapleton M., Schupski M.P., Smith T.,
RA Melson D.R., Wassarman D.A., Weinstock G.M., Wassenbach J.,
RA Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Science 297:2195-2195 (2000).
                                                             Misra S., Cr
Hradecky P.,
Smith C.D.,
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MEDLINE=22426070; Pubruc

Kaminker J.S., Bergman C.

Kaminker J.S., Wheel
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                                                                                                                                                                                                                                                                           Patel S., Frise E., Wheeler, Patel S., Frise E., Wheeler, Ashburner M., Celniker S.E.;
"The transposable elements of the
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Pacleb
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                                                                                                                                                            MEDLINE=22426069;
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MEDLINE=20196006;
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                             Crosby M.A., Mungall C.
P., Huang Y., Kaminker C.
P., Tupy J.L., Whitfied E
rt B.R., Celniker S.E.,
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PubMed=12537572;
M.A., Mungall C.J., Matthews B.B., Campbell K M.A., Kaminker J.S., Millburn G.H., Prochnik J.L., Whitfied B.J., Bayraktaroglu L., Bermar Celniker S.E., de Grey A.D., Drysdale R.A.,
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rgman C.M., Kronmiller
, Wheeler D.A., Lewis
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Best Local
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Q9VXU2; Q9601
01-MAY-2000
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Lewis S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inso
Neoptera; Endopterygota; Diptera; Brachycera;
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CG33206-PA (SD07366p).
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PROSITE; PS50913; GR1
SEQUENCE 1208 AA;
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Adams M.D., Celni
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                               SEQUENCE Stapleton M., BIUNE Stapleton M., Chavez C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E. Smith C.D., Tupy J.L., Whitfied B.Y., Bayraktarolu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spier B., Spradling A.C., Stapleton M., Strong R., Sun B., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong Y.H., Zhong F.M., Zhong W., Zhu S., Zhu X., Smith H., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22426070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller Patel S., Frise E., Wheeler D.A., Lewis
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                                                                                             FlyBase; FBgn0027287; 1(1)G0168.
InterPro; IPR000237; GRIP.
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enome Biol. 3:RESEARCH0084-RESEARCH0084(2002)
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Score 56; DB 2;
Pred. No. 3.9e+02;
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"IGR; BA1011".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22608414; PubMed-12721629; DOI-10.1038/nature01586; Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen Nelson K.E., Tettelin H., Fouts D.E., Bisen J.A., Gill S.R., Holtzapple B.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L. Colonay J.F., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Nelson W.C., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman W.C., Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O., Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O., Hazen A., Thomason B., Friedlander A.M., Koehler T.M.,
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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MEDLINE-22608414; PubMed=12721629;
Read T.D., Peterson S.N., Tourasse
Nelson K.E., Tettelin H., Fouts D.E.
Holtzapple E.K., Okstad O.A., Helgi
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Ol-JUN-2002 (TrEMBLrel. 21, Created)
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Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Transcriptional regulator, RpiR family.
OrderedLocusNames=Atu2598;
OrderedLocusNames=Atu2598;
                                                                                               Complete SEQUENCE
                                                                                                                                                                                     PIR; AE2895; AE2895.

PIR; H97670; H97670.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003705; P:carbohydrate metabolism; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajina J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Ruymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon I. Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon J. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL, CP000001; AAU19326.1; -.
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Brettin T.S., Bruce D.
Hitchcock P., Jackson
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhiz
Rhizobiaceae, Rhizobium/Agrobacterium group, Agroba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brettin T.S., Bruce D., Challacom
Hitchcock P., Jackson P., Keim P.
Richardson P., Rubin E., Tice H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
STRAIN=Dupont
                                                                                                                                                                                                                                                                                                                                                                           Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8UCA0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=288681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cereus ZK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                            "The
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Name=yhaN; ORFNames=BTZK0919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                       genome of the natural genetic
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AE009206; AAL43579.1; -.
                                                                                                                                                                             PF01380;
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287 AA;
                                                                                                                                         01380; SIS; 1.
PS00356; HTH_LACI_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAQEQLEEQE --- ENIRQIQKQMLADEERNT 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    974 AA;
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     Conservative
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                                                                                                  31331
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                       30.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Challacombe J.F.,
                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hallacombe J.F., Gilna
Keim P., Longmire J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 55.5; D; Pred. No. 3e+0
8; Mismatches
  Score 55; DB Pred. No. 90; 7; Mismatches
                                                                                                                                            UNKNOWN_1.
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                                              Length 287;
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Lucas S., Okinaka
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Perry M.,
Dolan M.,
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RESULT 29
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Best Local
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05-UUL-2004 (TrEMBLrel.
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AGR_C 4707p.
OrderedLocusNames=AGR_C
TISSUE=Placenta;

MEDLINB=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler R. R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F. Hopkins R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Hong L.,
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Science 294:2323-2328(2001).
EMBL, AE008173; AAK88221.; -.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0005700; F:transcription factor activity; IEA.
GO; GO:0005775; P:carbohydrate metabolism; IEA.
GO; GO:0006525; P:regulation of transcription, DNA-de
InterPro; IPR000843; HTH_LacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                         SEQUENCE
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InterPro; IPR009058; Wing_hlx_DNA_bnd.
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Agrobacterium tumefaciens C58.";
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PS00356; HTH LACI 1; UNKNOWN 1.
295 AA; 32258 WW; 3B50926B3CB72456 CRC64;
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QQRQRSMVTLRHIKQQLVEHRDPDDKQLLG
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Pred. No. 92;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Hsieh F.,
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C., Mullin L.,
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RESULT
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InterPro; IPR00128; RhoGAP.
InterPro; IPR00838; Rho GAP.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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TISSUE=P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=ARHGAP8;
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PROSITE; PS50238; RHOGAP; 1.
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Primates;
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4; Mismatches
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Best Local
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SMART; SMOO324; RhoGAP; I.
SMART; SMOO516; SEC14; I.
PROSITE; PS50191; CRAL TRIO; 1.
PROSITE; PS50238; RHOGAP; 1.
NON TER
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                                                                                                                                                                                                                                                                           Watanabe A., Iriguchi M., Kawashima Kiyokawa C., Kohara M. Matanaba Shimno C
                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                      -!- CATALYTIC ACTIVITY: Glutamy1-tRNA(Glu) + NADPH = glutamate-
semialdehyde + NADP(+) + tRNA(Glu).
-!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first st
Involved in chlorophyll biosynthesis.
-!- SIMILARITY: Belongs to the glutamy1-tRNA reductase family.
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          EMBL; AP005375;
HSSP; Q9UXR8; 10
                                                                                                                                                                                                                                           Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                              Name=hemA; OrderedLocusNames=tll1738;
Synechococcus elongatus (Thermosynechococcus
Bacteria; Cyanobacteria; Chroococcales; Synec
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                                DNA Res. 9:123-130(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Glutamyl-tRNA reductase (EC 1.2.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEM1_SYNEL
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Rodriguez A.C., Skalska U., So
                                                                                                                                                                                                                                                                                                                             MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                            STRAIN-BP-
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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InterPro; IPR001251; CRAL_TRIO_C.
InterPro; IPR000198; RhoGAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
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          1GPJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                        BAC09290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.1%;
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, Schmutz J., My
, Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB3921FA61C78C92 CRC64;
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                                                                                                                                                                                                                                                                                                                 Ikeuchi M.,
                                                                                                                                                                                                                                                                                                   <u>.</u>~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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(GluTR).
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                                                                                                                                                                                                                                                                                                   Kimura
                                                                                                                                                                                                                                                                                                                                                                                                 Synechococcus.
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7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                elongatus).
                                                                                                                                                                                                                                                                                                                Katoh
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                                                                                                                                                                                     first step.
                                                                                                                                                                                                                                                                                                                 Sasamoto
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
A Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Hopkins M., J., Wallan N., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,
A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Villalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Hodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Lones S.J. Maxra M. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O5-JUL-2004 (TrEMBLrel. 27, Last se 05-JUL-2004 (TrEMBLrel. 27, Last se Hypothetical protein (Fragment). Homo sapiens (Human). Eukaryota; Metaron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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Pfam; PF05201; GlutR N; 1.

Pfam; PF05200; GlutR NAD bind; 1.

TIGRFAMs; TIGR01035; hemā; 1.

PROSITE; P$00747; GLUTR; FALSE NEG.

Chlorophyll biosynthesis; Complete pr
Porphyrin biosynthesis; Complete pr
Porphyrin biosynthesis; Nucleoph
ACT_SITE 99 99 Proton A
InterPro; IPR00198; RhoGAP.
InterPro; IPR008936; Rho GAP.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00516; SEC14; 1.
PROSITE; PS50191; CRAL_TRIO; 1.
PROSITE; PS50238; RHOGAP; 1.
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Q6PJW1;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC010490; AAH10490.1; -.
HSSP; Q07960; 1AM4.
InterPro; IRR001251; CRAL TRIO C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                   IISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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InterPro; IPR000594; Thir domain.
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47596 MW;
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Primates;
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55.6%;
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Pred. No.
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Proton acceptor (By similarity).
, D84CE5A1D2AA777E CRC64;
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Catarrhini; Hominidae;
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annotation update)
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RESULT 33
Q8IZM6
ID Q8IZM
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Q86XV6
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                                                                                                            01-OCT-2000
AHRGAPB protein (Frayman)
Name=ARRGAPB;
Homo sapiens (Human)
Homo sapiens (Human)
Homo sapiens (Primates; Crarvota; Metazoa; Primates; Crarvota; Primates; Primates; Crarvota; Primates;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Q86XV6;
Q1-JUN-2003 (TrEMBLrel. 24, C
Q1-JUN-2003 (TrEMBLrel. 24, L
Q1-CCT-2003 (TrEMBLrel. 25, I
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01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00324; RhoGAP; 1.
SMART; SM00516; SEC14; 1.
PROSITE; P850191; CRAL TRIO; 1.
PROSITE; P850238; RHOGAP; 1.
SEQUENCE 433 AA; 49691 MW;
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NON TER 1
SEQUENCE 428 AA; 4
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HSSP; Q07960; 1RGP.
InterPro; IPR001251; CRAL_TRIO_C.
InterPro; IPR00198; RhoGAP.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BCH domain-containing Cdc42GAP-like protein.
                     SEQUENCE FROM N.A.
TISSUE=Colon;
MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000198; RhoGĀP.
InterPro; IPR008936; Rho_GAP
Pfam; PF00620; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shang X., Zhou Y.T., Low B.C.; "Concerted regulation of cell dynamics by BNIP-2 and Cdc44 homology/sec14p-like, proline-rich, and GTPase-activating domains of a novel Rho GTPase-activating protein, BPGAP1."
  Strausberg R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=22970011; PubMed=12944407; DOI=10.1074/jbc.M304514200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
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                                                                                                          NCBI_TaxID=9606;
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLRTEGLFRRSASVQTVREIQRL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLRTEGLFRRSASVQTVREIQRL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLSQEQLEHRERSLOTLRDIQRM 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem. 278:45903-45914(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
  Feingold E.A.,
PubMed=12477932; DOI=10.1073/pnas.242603899;
Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48607 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.1%;
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Last annotation updat
                                                                                                                                                                                                                                                                                         Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; I
Pred. No. 1.
                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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7;
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..4e+02;
7;
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; Homo.
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RHG8_HUMAN
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHG8 HUMAN STANDARD; PRT. Q9NGG0; O75983; O95695; Q96RW1; Q9Q9NXL1; Q9UH2O; 28-FEB-2003 (Rel. 41, Last sequence of the control                                                                                                                                                                                                                                   Gu J.R., wan D.F., Zh
Qin W.X., Huang Y., Q
Yu J., Han L.H.;
"Novel human cDNA clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=ARHGAP8;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50191; CRAL TRIO; 1.
PROSITE; PS50238; RHOGAP; 1.
NON TER
1
SEQUENCE 464 AA; 53142 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Alakek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.I., Marra M.A.
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

McDermid H.E., Hu S., Grundy P., Trichet V.;

McAttheward a putative tumor-suppressor gene on

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                growth.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                     Submitted (AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rho-GTPase-activating
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Altschul S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001251; CRAL TRIO C.
InterPro; IPR000198; RhoGAP.
InterPro; IPR008936; Rho GAP.
Pfiam; PF00620; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q07960; 1RGP.
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                                                                                                                                                                                                                                      human cDNA clones with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
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SM00516; SEC14; 1.
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                                                                                                                                                                                                                                                                                                                                                                        FROM
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Zeeberg
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                                                                                                                                                                                                                                                                                             (ISOFORM 4).

Zhao X.T., Zhou :
, Qiu X.K., Qian :
                                                                                                                                                                                                                                                                                                    Zhao
, Qiu
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Last annotation updat
protein 8 (PP610).
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                                                                                                                                                                 the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB
Pred. No. 1.5e
4; Mismatches
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                                                                                                                                                                     EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                               function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 718 AA.
L; Q96RW2; Q9HA49; Q9HC46; Q9NVX8;
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1.5e+02;
7;
                                                                                                                                                                                                                            of inhibiting cancer
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He L.P.,
                                  chromosome
      databases
                                                                                                                                                                     databases
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P., Li
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F
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H.N.,
                              22q13.3.";
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RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Wakamatsu A., Hayashi K., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J.-I., Saito K., Kawai Y., Isovanya T., Tanaka T., Ishii S.,

RA Yamamoto J.-I., Saito K., Kawai Y., Isovanya T., Wakamura Y.,

RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RA Sugawara M., Takahashi M., Kanda K., Yokii T., Furuya T., Kikawa E.,

ROmura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,

RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

RA Kusano J., Kanehori K., Takahashi-Pujii A., Hara H., Tanase T.-O.,

RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Suno S.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

"COmplete sequencing and characterization of 21,243 full-length human

"Complete sequencing and characterization of 21,243 full-length human
Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T., As Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M., A williams M., Wallis J.M., Whiteley M.N., Willey D.L., Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L., Williams L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Williams S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Roe B.A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., Rogers J., Shimizu N., A Roe B.A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., Rogers J., Shimia J., Shimia J., Lewis S., Lin S., P., Loh P., Hua A., Kenton S., Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., A Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L., A Wang Q., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Lao H., Bourne S., Murray J., Miller N., Minx P., Lao H., Bourne S., Murray J., Miller N., Minx P., Lao H., Bourne S., Murray J., Miller N., Minx P., Lao H., Bourne S., Murray J., Miller N., Minx P., Lao H., Bourne S., Murray J., Miller N., Minx P., Lao H., Bourne S., Millingham D., Willingham D.,
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Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
AR Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
AR Bagguley C., Baley S.E., Bridgeman A.M., Buck D., Burgess J.,
AR Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson B.,
AR Clegg S.M., Fleming K., French L., Garner A.A.,
Brans K.L., Fey J.M., Fleming K., French L., Garner A.G.,
AR Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
A Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
A Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
A Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
A Machay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
Delink B. W. Berger, V. Berger, V. Borger, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
Goward M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20057165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14702039; DOI=10.1038/ng1:
Ota T., Suzuki Y., Nishikawa T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10591208; DOI=10.1038/990031;
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Makita H.,
T., Ishii S
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EMBL; AF177331; AAG17975.1; -.
EMBL; AF195968; AAKS6136.1; -.
EMBL; AK195969; AAKS6137.1; -.
EMBL; AK000192; BAA99099.1; -.
EMBL; AK000192; BAA91614.1; -.
EMBL; AK022305; BAB14008.1; -.
EMBL; AK022305; BAB14008.1; -.
EMBL; AX022305; CAB1416.1; ALT_INIT.
EMBL; AS55192; CAB90248.1; -.
EMBL; Z93244; -; NOT_ANNOTATED_CDS.
EMBL; Z93244; -; NOT_ANNOTATED_CDS.
EMBL; Z93244; -; NOT_ANNOTATED_CDS.
EMBL; Z93244; -; NOT_ANNOTATED_CDS.
EMBL; Z93246; B59436.
                                        Pfam; PF00620; RhoGAP; 1.
PROSITE; PS50191; CRAL TRIO; 1.
PROSITE; PS50138; RHOGAP; 1.
Alternative splicing; GTPase acti
DOMAIN
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CRAL
DOMAIN
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Rho-
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Miss
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Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.
Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J.
Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.
O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
Wilson R.S., Lane L., Tilahun Y., Wright H.;
Wilson BNA sequence of human chromosome 22.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                    Genew; HGNC:677; ARHGAPB.
InterPro; IPR0001251; CRAL TRI(
InterPro; IPR000936; Rho-GAP.
InterPro; IPR000198; Rho-GAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                                                     HSSP; Q07960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 CRAL-TRĪO domain. SIMILARITY: Contains 1 Rho-GAP domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=4;
IsoId=Q9NSG0-5;
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Comment=Additional isoforms seem to exist. Full isoforms so
detected are isoforms 1 to 7. Experimental confirmation may
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VSP_001655;
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VSP_001654;
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VSP_001657;
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Rho-GAP.
Missing (in isoform
/FTId=VSP_001645.
                                                                                           activation. CRAL-TRIO.
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                        Kemp P.R., Cooper W.N
"MASH3 a novel basic
in C2C12 cells.";
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Achaete-scute homolog 3 (bHLH transcriptional
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                                                                                               "Sgn1, a basic helix-loop-helix transcription salivary gland duct cell lineage in mice."; Dev. Biol. 240:517-530(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Amid C., Bahr A.,
Zabel B., Hankeln
                     MEDLINE=21418998;
Amid C., Bahr A.,
                                                                                                                                                                                                STRAIN=C57BL/6;
MEDLINE=21643927;
                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Ascl3; Synonyms=Mash3, Sgn1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JJR7;
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  Hankeln
                                                                                                                                                                                                                                                                                       (APR-2000)
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                                                                                                                                                                                 Ohbo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
Mujica A., Sampson T., Schmidt E.R.;
                                                                                                                                                                                 PubMed=11784080; DOI=10.1006/dbio.2001.0473;
K., Takakura A., Takebayashi H., Okada T., Ab
                                       PubMed=11528127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388
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                                                                                                                                                                                                                                                                                                                                helix-loop-helix protein that inhibits myogenesis
                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                    Metcalfe J
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Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoro /FTId=VSP_001654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKKNLKALYVHPTSFIKVLMNILKPLISHKFGKKVIYFNY
LSELHEHLKYDQLVIPPEVLRYDEK -> QEPPCQANTLVL
KGPDSQHFSFAGLLIYCNNSAGLCSSKTLWTLKCEFHVIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHEIFFCFFFSTT (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_001651.
Missing (In isoform 1 and
/FTId=VSP_001652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoform 4 and isoform 7).
/FTId=VSP_001650.
Missing (In isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDSEGIFIDFGRGRGSGMSDLEGSGGRQSVV
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TSIRRHSVSEMTSCPEPQGFSDPPGQGPTGTFRSSPAPHSG
PCPSRLYPTTQPPEQGLDPTRSSLPRSSPENLVDQILESVD
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RHGILQVAGDDRFGBRVVTFSCCRWPSHELDHQRLESYLK
YYILDQYVENDYTIVYFHYGLNSRNKPSLGWLQSAYKEFDRK
DGDLTMWPRLVSNSKLKRSSHLSLPKYWDYRYKK -> KRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (In isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP_001647.
KIRFYE -> MAPMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (In isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP_001653.
Missing (in isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulator Sgn-1) (Mash-
                                                                                                                                            factor delineates the
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                   S.E.,
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RESULT 37
PHYMB ORYSA
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DT 01-MAY
DT 01-MAY
DT 05-JUL
DE Phytoc
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OC Enkary
OC Sperma
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Best Local S
Matches 13
                    STRAIN=cv. Indica / IR36; TISSUE=Seedling shoot;

MEDLINE=91172131; PubMed=2005872;

Dehesh K., Tepperman J., Christensen A.H., Quail P.H.;

"phyB is evolutionarily conserved and constitutively expressed in rice seedling shoots.";

Mol. Gen. Genet. 225:305-313(1991).

"FUNCTION: Regulatory photoreceptor which exists in two forms that are reversibly interconvertible by light: the Pr form that absorbs maximally in the red region of the spectrum and the Pfr form that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P25764;
01-MAY-1992
01-MAY-1992
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMĀIN
SEQUENCE
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between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=PHYB; Synonyms=PHYB1;
Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by modified
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Cytogenet. Cell Genet. 93:284-290(ZUUL).

-!- FUNCTION: Transcriptional repressor. Inhibits myogenesis.
-!- FUNCTION: Transcriptional requires dimerization with
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MGI:1928820; Ascl3.
GO:0005634; C:nucleus; IDA.
GO:0005667; C:transcription factor complex; IPI.
GO:0003677; F:DNA binding; IDA.
GO:0005515; F:protein binding; IPI.
GO:003528; F:transcription regulator activity; IDA.
GO:006357; P:regulation of transcription from Pol II pro. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Specifically expressed in the salivary
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(Rel. 22,
(Rel. 44,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: Nuclear.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Repressor; Transcription Basic motif. Helix-loop-helix motif.
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r form c
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Q84LN8; Q84LN8; 01-JUN-2003 01-JUN-2003 01-MAR-2004 Phytochrome

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

24,

Created) Last sequ

sequence

update)

Last annotation update)

PRELIMINARY;

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Name=PHYB;

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RESULT
Q84LN8
ID Q8
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                                                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO0229; sensory_box; 2
PROSITE; PS50109; HIS KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS00245; PHYTOCHROME_1; 1.
PROSITE; PS50046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; HisKA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Contains one covalently linked tetrapyrrole chromophore.
-!- SIMILARITY: Belongs to the phytochrome family.
-!- SIMILARITY: Contains 1 histidine kinase domain.
-!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domain
                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                     Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gramene; P25764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X57563; CAA40795.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement
                                                                                                                                                                                                                                                                                                          Franscription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                             38
                                                                                                                                   1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            responses. Pfr controls the expression of a number of nuclear genes including those encoding the small subunit of ribulose-bisphosphate carboxylase, chlorophyll A/B binding protein, protochlorophyllide reductase, rRNA, etc. It also controls the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protochlorophyllide reductase, rR expression of its own gene(s) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfr induces an array of morphogenic responses, whereas reconversion of Pfr to Pr cancels the induction of those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     absorbs maximally in the far-red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S14065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00989; PAS; 2.
PF00360; Phytochrome; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02518; HATPase c. PF00512; Hiska; T.
                                                                                                                                                          ω
                                                                                                                                                                                 l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             SM00091;
                                                                                                                                   VSQVMIQLRERDLQLIRDI-----
                                                                                                                                                     LSQEQLEHRERSLQTLRDIQRMLFPDE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003594;
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                                                                                                                                                                                                                                                                    661
795
943
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                   Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S14065.
                                                                                                                                                                                                                                                                                                      regulation.
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                                                                                                                                                                                                                                                                                                                                                                                           PAS; 2.
                                                                                                                                                                                                                                 A,
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866
1161
51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              institutions as long as its content tatement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAF.
His_kinase.
His_kinA_N.
                                                                                                                                                                                           29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phytochrome
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                                                                                                                                                                                                                                 128384
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                                                                                                                                                                                      PAS 1.

PAS 2.

Histidine kinase.

Histidine kinase.

Chromophore (By similarity).

CMW; E8292E88B769BF16 CRC64;

DB 1; Length
                                                                                                                                                                                 4.
                                                                                                                                                                                Score 54.5; DB
Pred. No. 5e+02;
4; Mismatches
                                                                                                                                                                                                                                                                                                                    Photoreceptor;
                                                                                                                                  PDE 1040
                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rRNA, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region. Photoconversion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  moved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                   Phytochrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   feedback
                                                                                                                                                                                                        Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domains.
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RESULT 39
Q6D1R6
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Best Local 9
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InterPro; IPR000977; DNA ligase.
InterPro; IPR0009077; His kinase.
InterPro; IPR005467; His kinase.
InterPro; IPR003661; His kina.
InterPro; IPR001691; PAS.
InterPro; IPR001294; Phytochrome.
InterPro; IPR001294; Phytochrome.
InterPro; IPR001690; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PP02518; HATPASE C; 1.
Pfam; PP00512; HisKA; Ī.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; Phytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00387; HATPASE C; 1.
SMART; SM00388; HisKA; Ī.
SMART; SM00381; HisKA; Ī.
SMART; SM00391; PAS; 2.
                                                                                                                                                                                                                Q6D1R6
Q6D1R6;
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence upd
26-OCT-2004 (TrEMBLrel. 28, Last sequence upd
26-OCT-2004 (TrEMBLrel. 28, Last sequence update
26-OCT-2004 (
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                        Enterobacteriaceae; Pectobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01590; GAF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tahir M., Kanegae H., Takano M.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=39947,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0000155; P:two-component sensor molecule activity; IEA. GO:0018298; P:protein-chromophore linkage; IEA. GO:0009585; P:red, far-red light phototransduction; IEA. GO:0006585; P:regulation of transcription, DNA-dependent; IEA. GO:00067165; P:signal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005524; F:ATP binding; IEA.
GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
GO:0016301; F:kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0007601; P:visual perception;
                                                                                                                                                                                                                                                                                                                                                                                        1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M8; TIGR00229; sensory_box; 1.

E; PS00697; DNA_LIGASE_A1; UNKNOWN_1.

E; PS50119; HIS_KIN; 1.

E; PS50112; PAS; 2.

E; PS50145; PHYTOCHROME_1; 1.

E; PS500445; PHYTOCHROME_2; 1.

E; PS500445; WD_REPEATS_1; UNKNOWN_1.

E; PS00676; WD_REPEATS_1; UNKNOWN_1.

E; PS00676; WD_REPEATS_1; UNKNOWN_1.

E; PS00676; WD_REPEATS_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   LSQEQLEHRERSLQTLRDIQRMLFPDE 29
                                                                                                                                                                                                                                                                                                                                                                                     VSQVMIQLRERDLQLIRDI ---- PDE 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.8%;
48.1%;
                                                                                                                                                                28, Created)
28, Last sequence update)
28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54.5; DB Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEE981FC89D46FDC CRC64;
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                                                                                              (Pectobacterium atrosepticum)
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                                                                       Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 40
Q7R1P0
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PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell'K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.C.C., Mungall K.,
Atkin R., Bason N., Brooke K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
carottovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7R1P0;
01-MAR-2004
01-MAR-2004
                                                                                                                                                                                      GO; GO:0006468; p:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase_like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000721; Ser thr_pkin_AS.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 554 AA; 62825 MW; 0A159E951BD36EF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).

EMBL; BX950851; CAG76279.1; -.

InterPro; IPR007817; DIT1_PvcA.

Pfam; PF05141; DIT1_PvcA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity;
GO; GO:0016740; F:transferase activity; IEA.
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Giardia lamblia ATCC 50803.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. 18 derived by analysis of the total score distribution.

Result

Query

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AAG63852	AAG63851	AAB68522	ABG96285	ADP56605	ADP56606	ADM83551	ADQ74859	ABR82444	AAB95073	ADP56608	ADP56607	ABU17570	ABB63502	ADQ17519	ADL83239	ADM26229	ADN19362	ADK63408	ABR53351
Aag63852	Aag63851	Aab68522	Abg96285	Adp56605	Adp56606	Adm83551	Adq74859	Abr82444	Aab95073	Adp56608	Adp56607	Abu17570	Abb63502	Adq17519	Ad183239	Adm26229	Adn19362	Adk63408	Abr53351
Amino aci	Amino aci	Human GTP	Human ova	Human bre	Human bre	Human	Human	Human	Human pro	Human bre	Human bre	Protein	Drosophi]	Human sof	Human PRC	Hyperther	Bacterial	Disease	Protein

ALIGNMENTS

Human soft tissue sarcoma-upregulated protein - SEQ ID 1764

soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue

Example 2; SEQ ID NO 1764; 210pp; English.

RESULT 1
ADQ18945
ID ADQ18945 standard; protein; 1394 AA
XX
AC ADQ18945;
XX
DT 26-AUG-2004 (first entry)
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulate
XX
DE Human soft tissue sarcoma; cytostatic; gen
XX
DE Human soft tissue sarcoma;
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DE Human soft tissue sarcoma
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DE Human soft tissue sarcoma
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DE 26-NOV-2003; 2003WO-US038193.
XX
DE 26-NOV-2003; 2002US-0429739P.
XX
DE 26-NOV-2002; 2002US-0429739P.
XX
DE AZIZ N, Ginsburg WM, Zlotnik A;
XX
DE AZIZ N, Ginsburg WM, Zlotnik A;
XX
DE AZIZ N, Ginsburg WM, Zlotnik A;
XX
DE WPT; 2004-441208/41.
XX
DE AZIZ N, Ginsburg WM, Zlotnik A;
XX
DE AZIZ N, Ginsburg WM, Zlotn The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

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RESULT 2
AAB71229
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                                                                                       This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legiss (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the human legless (1gs) protein homologue lgs/bcl9 described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Legless; human; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast, head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                      Sequence 1426
                                                                                 disclosure
                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF88467.
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    36;
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                                                                                                                                                                                                                                                                    II; Fig 8B; 41pp; English
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100.0%; Score 183; DB 5
100.0%; Pred. No. 6e-16;
tive 0; Mismatches
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RESULT 4
ADJ70152
ID ADJ7
XX
AC ADJ7
XX

ADJ70152 standard;

protein; 1426 AA

ADJ70152

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RESULT 3
ABMO1534
ID ABMO
XX ABMO
AC ABMO
XX ABMO
XX Leg]
XX Leg]
XX Leg]
XX US2C
XX Homc
XX Homc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000; 2000US-0221502P.
27-JUL-2001; 2001US-00915543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; tissue regeneration; tissue repair; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Legless protein; lgs; cell fate disorder; blood disease; gene therapy;
                                                                                                                                          госат
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                                                                                                                Conservative
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                                                                                                                                    Score 183; DB 7
Pred. No. 6e-16;
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                                                                                                                                                                  Length 1426;
                                                                                                          Indels
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RESULT
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Best Local (
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                            altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug soreening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELRS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, antiarthritic, osteopathic, ophthalmological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2002; 2002US-0372843P
17-JUN-2002; 2002US-0389987P
20-SEP-2002; 2002US-0412418P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial; human;
Huntington's disease;
Leber's hereditary opt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises detecting a modified polypeptide in a sample with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                   Sequence 1426 AA;
                                                                                                                                                                                                                                                                                                 cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1958; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2003.
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20-MAY-2004
                             ADJ71903;
                                                             ADJ71903 standard; protein; 1426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tor therapeutic intervention in treating a disease associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel mitochondrial targets that can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BUCK-) BUCK INST AGE RES
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                                                                                                                                                                     μ
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                                                                                                                                                         DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQ 36
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                                                                                                                                                                                                    Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В,
                                                                                                                                                                                                    0;
                                                                                                                                                                                                                   Score 183; DB 7
Pred. No. 6e-16;
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                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                  DB 7;
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                                                                                                                                                                                                                                    Length 1426;
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RESULT 6
ABB11808
ID ABB1
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ABB11808 standard; peptide; 1435 AA

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                                                                                                                                                                                                      cc amino acid domains with a Legless (Lgs) protein and is therefore a contract and homologue of Lgs. The invention also relates to a nucleotide sequence encoding a protein present in invertebrate and/or vertebrate cc organisms, the nucleotide sequence encoding a protein comprising a corpositive function in a regulatory pathway and the use of the polypeptide for the isolation of Lgs-binding proteins by carrying out an assay chosen cc from an in vitro binding assay with such a peptide or a co-cimmunoprecipitation from vertebrate or invertebrate cell lysates or a comammalian or yeast two hybrid assay. The polypeptide and polynucleotide are useful for treating disorders of cell fate, which involves administering therapeutic compounds chosen from invertebrate and cyrrebrate Lgs protein homologues or fragments, antibodies, antibody crarebrate Jgs antisense DNA, lgs antisense RNA, lgs double-stranded RNA, care related to cell differentiation or cell proliferation. The disorders are related to cell differentiation or cell proliferation. The disorders are related to cell differentiation or cell proliferation. The disorders are related to treat a cancerous condition by preventing progression from a pre-neoplastic or non-malignant condition to a neoplastic or stimulation of the Wnt pathway and is medulloblastoma or cancer of the compound may also be administered to a blood disease to promote tissue colon, breast, head and neck, brain, thyroid or skin. The therapeutic colon, when the compound condition are represented to tissue tregeneration and repair. This sequence represents the human Lgs/Bc19
                                                                          Matches
                                                                                                               Query Match
                                                                                                                                                     Sequence 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptide sharing one or more homologue amino acid domains with Legless protein being functional homologue of Legless, useful for diagnosing disorders of cell fate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; legless; lgs; cell differentiation disorder; cell proliferation disorder; cancer; wnt pathway; medulloblastoma; colon; breast; head; neck; brain; thyroid; skin; blood disease; tissue regeneration; tissue repair; cytostatic; Lgs/Bc19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a polypeptide sharing one or more homologous amino acid domains with a Legless (Lgs) protein and is therefore a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Basler
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27-JUL-2001; 2001US-00915543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Lgs/Bc19 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; SEQ ID NO 15; 62pp; English.
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                                                                                             Local
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                                                                                           Similarity
                  DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQ 36
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                                                                                                                                                                                              of the
                                                                                                                                                         Ä
                                                                                                                                                                                                invention.
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                                                                        Score 183; D
Pred. No. 6e-
D; Mismatches
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                                                                                         6e-16;
                                                                                                                 DB 8;
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                                                                                                             Length 1426;
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thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby
                                                                                                                                                                                                                                                                                                                                 giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; hammanopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activity. or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; ostcopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
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27-APR-2000; 2000US-00560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vulnerary; antiulcer
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immunomodulator; activin;
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RESULT 7
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XX Huma
XX Huma
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Best Local
organisms, the nucleotide sequence encoding a protein comprising a positive function in a regulatory pathway and the use of the polypeptide for the isolation of Igs-bindary proteins by carrying out an assay chosen from an in vitro binding assay with such a peptide or a communoprecipitation from vertebrate or invertebrate cell lysates or a mammalian or yeast two hybrid assay. The polypeptide and polynucleotide are useful for treating disorders of cell fate, which involves administering therapeutic compounds chosen from invertebrate and vertebrate Igs protein homologues or fragments, antibodies, antibody fragments, 1gs antisense NNA, 1gs double-stranded NNA, 1gs antisense NNA, 1gs antisense NNA, 1gs double-stranded NNA, 1gs double-st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid domains with a Legless (Lgs) protein and is therefore a functional homologue of Lgs. The invention also relates to a nucleotide seguence encoding a protein present in invertebrate and/or vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000US-0221502P
27-JUL-2001; 2001US-00915543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide sharing one or more homologue amino acid domains with Legless protein being functional homologue of Legless, useful for diagnosing disorders of cell fate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Basler K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004038901-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening techniques. The present sequence represents a novel human polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a polypeptide sharing one or more homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-2003; 2003US-00664859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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Mo. 6e-16;
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                                                                                                                                                                                                                                                            The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear localised protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                         Sequence 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 91-92; 113pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New beta-catenin nuclear diseases associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse beta-catenin nuclear localised protein
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                                                                                                                        Similarity
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                                                                                                                        59.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      localized protein for diagnosis and treatment nuclear localization of beta-catenin e.g.
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                                                                                       Score 109; DB Pred. No. 1.7e 4; Mismatches
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RESULT 10 AAU78463 ID AAU78

AAU78463 standard; protein;

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Mouse; beta-catenin nuclear expressed sequence tag.

localised protein;

cancer; gene therapy;

EST;

Human beta-catenin nuclear localised protein #2.

02-JUL-2002 AAU78463;

(first entry)

WO200224738-A1 Homo sapiens.

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RESULT 9
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                                              Matches
                                                         Query Match
Best Local
                                                                                                                            The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                WO200224738-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU78460;
                                                                                            Sequence 1494 AA;
                                                                                                                                                                                                    Claim 1; Page 81-88; 113pp; Japanese.
                                                                                                                                                                                                                                       New beta-catenin nuclear localized protein for diagnosis and treatment diseases associated with nuclear localization of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                              Akiyama T,
                                                                                                                                                                                                                                                                                                                                                             22-SEP-2000; 2000JP-00287876
                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse beta-catenin nuclear localised protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78460
                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2001; 2001WO-JP008140.
                                                                                                                  localised protein
                                                                                                                                                                                                                                                                                                                                    (КУОМ ) КУОМА НАККО КОСУО КК
                                                         Local Similarity
                                                                                                                                                                                                                                                                                      2002-330014/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
394 EGLSKEQLEHRERSLQTLRDIERLL 418
             1 DGLSQEQLEHRERSLQTLRDIQRML 25
                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-catenin nuclear localised protein;
                                                                                                                                                                                                                                                                           ABK47631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; protein; 1494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGLSKEQLEHRERSLQTLRDIERLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                            Conservative
                                                                                                                                                                                                                                                                                                              Adachi S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tag.
                                                       59.6%;
                                            4;
                                                       Score 109; DB 5;
Pred. No. 9.3e-06;
                                              Mismatches
                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                   Length 1494;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy;
                                            0
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST;
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RESULT 11
AAB71230
ID AAB71
XX AB71
XX AB71
XX IB-NC
XX Legle
XW Lissu
XW blood
XW medul
XX medul
XX Medul
XX ISSU
PP 27-JU
XX (BASI
PA (BASI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Legless; human; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of human beta-catenin nuclear localised protein #2
  N-PSDB;
                                                                                                                                                                                                                                                        28-JUL-2000; 2000US-0221502P
                                                                                                                                                                                                                                                                                                      27-JUL-2001; 2001US-00915543
                                                                                                                                                                                                                                                                                                                                                      04-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           medulloblastoma; skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human legless homologue hlgs-1 partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New beta-catenin nuclear diseases associated with
                                                                   Basler
                                                                                                                                                                                                                                                                                                                                                                                                 US2002086986-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB71230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB71230 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 102-105; 113pp; Japanese
                                                                                                                                                               (FROE/)
                                                                                                                                                                                    (BRUN/)
                                                                                                                                                                                                          (BASL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2002
                        2002-635689/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-330014/36
DB; ABK47638.
                                                                   <u>,</u>~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                              BRUNNER E. FROESCH B. KRAMPS T. PETER O.
  AAF88468
                                                                                                                                                                                                            BASLER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          куома накко косуо кк
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLSKEQLEHRERSLQTLRDIERLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLSQEQLEHRERSLQTLRDIQRML 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         738
                                                                   Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%; ilarity 87.5%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adachi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000JP-00287876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-JP008140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; tissue
                                                                   Froesch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     localized protein for diagnosis and treatment nuclear localization of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 107; DB 5
Pred. No. 8e-06;
3; Mismatches
                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                   Kramps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                   Ţ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                   Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          윥
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                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                        Legless cancer;
                                                         Novel Lgs polypeptide useful diagnosing disorders of cell
                                                                                                                         28-JUL-2000; 2000US-0221502P.
27-JUL-2001; 2001US-00915543.
                                                                                                                                                                                                                                                                                                                                         Sequence
                                             Claim
                                                                                                                                            19-DEC-2002; 2002US-00322579
                                                                                                                                                         19-JUN-2003
                                                                                                                                                                     US2003114413-A1
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                 Human lgs-1
                                                                                                                                                                                                                              15-JAN-2004
                                                                                                                                                                                                                                                       ABW01535
                                                                                                            (UYZU-) UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nove1
                                                                                                                                                                                                                                                                                                                      Local
                                                                                  2003-829432/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          fate
                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide useful in therapeutic method for treating disorders fate such as cell differentiation or cell proliferation.
                                                                                                                                                                                                                                                                                       76
                                                                                                                                                                                              protein;
tissue re
                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                     invention
                                                                             AAD62643
                                                                                                                                                                                                                                                                                                                      Similarity
                                             Fig 10B; 0pp;
                                                                                                                                                                                                                                                                                                  GLSQEQLEHRERSLQTLRDIQRML
                                                                                                                                                                                                                                                                                                                                         1115
                                                                                                                                                                                                                                                       standard; protein; 1115
                                                                                                                                                                                                                                                                                       GLSKEQLEHRERSLQTLRDIERLL
                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                         Ā
                                                                                                                                                                                              regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                             10B;
                                                                                                                                                                                                    lgs;
                                                                                               Ŋ
                                                                                                                                                                                                                                                                                                                                                           protein homologue hlgs-1 described in the disclosure
                                                                                                                                                                                                                                                                                                                    58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            41pp;
                                                                                                                                                                                                    cell fate
                                             English.
                                                                                                Froesch
                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                              Score 107; DB 5;
Pred. No. 1.3e-05;
3; Mismatches (
                                                         for isolation fate, treating
                                                                                                                                                                                              tissue
                                                                                               'n
                                                                                                                                                                                                    disorder; blood disease;
                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                  25
                                                         treating
                                                                                               Kramps
                                                                                                                                                                                              repair; cytostatic
                                                                                               H
                                                         of Lgs-binding
g diseases such
                                                                                                Peter
                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                               Indels
                                                                                               0
                                                                                                                                                                                                                                                                                                                            1115;
                                                                                                                                                                                                    gene therapy;
                                                         proteins,
                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of.
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The invention relates to novel legless (lgs) proteins and polynucleotides encoding such proteins. Lgs sequences are useful for the treatment of disorders of cell fate such as differentiation or proliferation. The invention is used to treat blood disease or a cancerous condition characterised by over-stimulation of the Wnt pathway such as colon,

over-stimulation of neck, brain, thyroi

thyroid,

ne Wnt pathway such medulloblastoma or

as colon, skin canc

and

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RESULT 13
ADJ71905
ID ADJ71905
AC ADJ71
XX ADJ71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
The invention relates to a polypeptide sharing one or more homologous amino acid domains with a Legless (Lgs) protein and is therefore a functional homologue of Lgs. The invention also relates to a nucleotide sequence encoding a protein present in invertebrate and/or vertebrate organisms, the nucleotide sequence encoding a protein comprising a positive function in a regulatory pathway and the use of the polypeptide for the isolation of Lgs-binding proteins by carrying out an assay chosen from an in vitro binding assay with such a peptide or a communoprecipitation from vertebrate or invertebrate cell lysates or a mammalian or yeast two hybrid assay. The polypeptide and polynucleotide are useful for treating disorders of cell fate, which involves administering therapeutic compounds chosen from invertebrate and vertebrate Lgs protein homologues or fragments, antibodies, antibodies, antibodies, antibodies, antibodies, antibodies consenses RNA, lgs antisense RNA, lgs antisense RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is administered to prevent progression from a pre-neoplastic or non-malignant condition to a neoplastic or malignant state. It is administered to promote tissue regeneration and repair. The invention is also useful in the therapy of diseases cost by an over-activation of Wg pathway. It is useful for reducing 1gs gene expression in an invertebrate or vertebrate organism or an invertebrate or vertebrate organism or an invertebrate or vertebrate cell line. The invention is also useful in gene therapy. The present sequence is human 1gs-1 protein used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptide sharing one or more homologue amino acid domains
Legless protein being functional homologue of Legless, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000;
27-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-203288/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Basler K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004038901-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; legless; lgs; cell differentiation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ71905 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYZU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-2003; 2003US-00664859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Lgs/Bc19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation disorder; cancer; Wnt pathway; medulloblastoma; colon;
st; head; neck; brain; thyroid; skin; blood disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLSKEQLEHRERSLQTLRDIERLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLSQEQLEHRERSLQTLRDIQRML 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0221502P
2001US-00915543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     partial polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of cell fate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Froesch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62pp; English
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Pred. No. 1.3e-05;
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              The invention relates to novel legless (1gs) proteins and polynucleotides encoding such proteins. Lgs sequences are useful for the treatment of disorders of cell fate such as differentiation or proliferation. The invention is used to treat blood disease or a cancerous condition characterised by over-stimulation of the Wnt pathway such as colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer and is administered to prevent progression from a pre-neoplastic or non-malignant condition to a neoplastic or malignant state. It is administered to promote tissue regeneration and repair. The invention is also useful in the therapy of diseases cost by an over-activation of Wg pathway. It is useful for reducing 1gs gene expression in an invertebrate or vertebrate organism or an invertebrate or vertebrate cell line. The invention is also useful in gene therapy. The present sequence is Drosophila species legless (1gs) peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interfering with Lgs function, synthesis and degradation. The disorders are related to cell differentiation or cell proliferation. The compound is administered to treat a cancerous condition by preventing progression from a pre-neoplastic or non-malignant condition to a neoplastic or malignant state. The cancerous condition is characterised by overstimulation of the Wnt pathway and is medulloblastoma or cancer of the colon, breast, head and neck, brain, thyroid or skin. The therapeutic compound may also be administered to a blood disease to promote tissue regeneration and repair. This sequence represents a human Lgs/Bc19 partial polypeptide of the invention.
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27-JUL-2001;
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                                                                                                                                                                                                                                                                                                                  Claim
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2001US-00915543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 107; DB 8;
Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       В,
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CC amino acid domains with a Legless (Lgs) protein and is therefore a CC functional homologue of Lgs. The invention also relates to a nucleotide sequence encoding a protein present in invertebrate and/or vertebrate CC organisms, the nucleotide sequence encoding a protein present in invertebrate and/or vertebrate CC organisms, the nucleotide sequence encoding a protein comprising a CC positive function in a regulatory pathway and the use of the polypeptide CC for the isolation of Lgs-binding proteins by carrying out an assay chosen CC immunoprecipitation from vertebrate or invertebrate cell lysates or a CC mammalian or yeast two hybrid assay. The polypeptide and polynucleotide are useful for treating disorders of cell fate, which involves CC are useful for treating disorders of cell fate, which involves CC ragments, lgs antisense NNA, lgs antisense RNA, lgs double-stranded RNA, conterfering with Lgs function, synthesis and degradation. The disorders is administered to treat a cancerous condition by preventing progression CC malignant state. The cancerous condition is characterised by overcc stimulation of the Wnt pathway and is medulloblastoma or cancer of the CC compound may also be administered to brain, thyroid or skin. The therapeutic compound may also be administered to a concer of the CC compound may also be administered to a concer of the CC compound may also be administered to a concer of the CC compound may also be administered to a concer of the concernes of the concer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptide sharing one or more homologue amino acid domains with Legless protein being functional homologue of Legless, useful for diagnosing disorders of cell fate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Basler K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000US-0221502P.
27-JUL-2001; 2001US-00915543:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a polypeptide sharing one or more homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4; 62pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fruit fly legless (lgs) peptide fragment
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sequence represents a Drosophila
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Best Local Similarity
                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                    Sequence 1429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 3129; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB58779 standard; protein; 1429
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                                                                                                                                                                    from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                Local
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                                Similarity
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                             Score 66; DB
Pred. No. 7.1;
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Pred. No. 0.12;
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                                                     DB 4; Length 1429;
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RESULT 18
ABW01527
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the Drosophila melanogaster (fruitfly) legless (lgs) protein described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (lgs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling path
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1464 AA;
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                             15-JAN-2004
                                                                                    ABW01527;
                                                                                                                                        ABW01527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide useful in therapeutic method for treating disorders of fate such as cell differentiation or cell proliferation.
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BRUNNER E.
FROESCH B.
KRAMPS T.
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                                                                                                                                        standard;
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                             (first entry)
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31.4%;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB Pred. No. 7.3;
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RESULT 19
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also useful in the therapy of diseases cost by an over-activation of Wg pathway. It is useful for reducing 1gs gene expression in an invertebrate or vertebrate organism or an invertebrate or vertebrate cell line. The invention is also useful in gene therapy. The present sequence is Drosophila species legless (1gs) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel legless (19s) proteins and polynucleotides encoding such proteins. Lgs sequences are useful for the treatment of disorders of cell fate such as differentiation or proliferation. The invention is used to treat blood disease or a cancerous condition characterised by over-stimulation of the Wht pathway such as colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer and is administered to prevent progression from a pre-neoplastic or nonmalignant condition to a neoplastic or malignant state. It is administered to promote tissue regeneration and repair. The invention is
                                                                            Fruit fly, legless; lgs; cell differentiation disorder; cell proliferation disorder; cancer; wnt pathway; medulloblastoma; colon; breast; head; neck; brain; thyroid; skin; blood disease; tissue regeneration; tissue repair; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1464 AA;
                                                                                                                                                                                           20-MAY-2004 (first entry)
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                                               Drosophila melanogaster
                                                                                                                                                           Fruit fly legless (lgs) polypeptide.
                                                                                                                                                                                                                                                          ADJ71911 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Fig 2; Opp; English.
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27-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                          DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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2001US-00915543.
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                                                                                                                                                                                                                                                        protein; 1464 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB Pred. No. 7.3;
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Best Local
           Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; nephrotropic; antithyroid; cerebroprotective; antiparkinsonian; anticonvulsant; MDDT; nootropic; neuroprotective; antidiabetic; gene therapy; atherosclerosis; molecule for disease detection and treatment; cancer; AIDS; allergy; diabetes; glomerulonephritis; autoimmune thyroiditis; Cushing's syndrome
                                                                                                                                  Human molecule
                                                                                                                                                                        24-JUL-2003
                                                                                                                                                                                                                                                 ABP98879 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptide sharing one or more homologue amino acid domains Legless protein being functional homologue of Legless, useful for diagnosing disorders of cell fate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid domains with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 1; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Basler K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYZU-) UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000;
27-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-2003;
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                                                                                                                                                                                                                                                                                                                                              515
                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
 Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                              ENLTPOOROHREEQLAKIKKMNQFLFPENENSVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                    (first entry)
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2001US-00915543
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                                                                                                                              for disease detection and treatment MDDT-7.
                                                                                                                                                                                                                                             protein; 1014 AA.
disease; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                       36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Froesch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o a polypeptide sharing one or more homolo a Legless (Lgs) protein and is therefore
                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB (
Pred. No. 7.3;
LO; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1464;
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               syndrome,
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RESULT 21
ABJ75853
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ID ABJ7
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26-OCT-2001;
02-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease detection and treatment" (MDDT) and genes encoding them. The invention also includes molecule which are at least 90% identical to the protein and nucleotide sequences. This sequence represents a protein of the invention. Disorders associated with aberrant expression of MDDT, a cell proliferative disorders (e.g. cancer or atherosclerosis), autoimmune/inflammatory disorders (e.g. AIDS, allergies, diabetes, glomerulomephritis or autoimmune thyroiditis), developmental disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Forsythe IJ, Emerling BM, Hafalia AJA, Yue H, Xu Gietzen KJ, Chawla NK, Baughn MR, Marquis JP, Becha SD, Ka Lal PG, Richardson TW, Lee SY, Lee EA, Tran B, Warren BA, Gururajan R, Sprague WW, Blake JJ, Thangavelu K, Swarmakar Gorvad AE, Griffin JA, Lindquist EA, Elliott VS, Ison CH;
                                                                                                                                                                                Fungicide; cytostatic;
                                                                                                                                                                                                                                                                                          16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1014 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated peptide molecules for disease for diagnosing, treating or preventing atherosclerosis, diabetes or stroke.
                                                                                                    Aspergillus
                                                                                                                                                                                                                                      Aspergillus
                                                                                                                                                                                                                                                                                                                                              АВJ25853
                                                                                                                                                                                                                                                                                                                                                                                            ABJ25853 standard; protein; 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (e.g. Cushii
Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 151-153; 234pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the isolation of a number of "molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cushing's syndrome) or neurological disorders (e.g. stroke, nson's disease or epilepsy)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                        contamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACC44394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKHKDRTM-NLQDIRYILKNDLKDFTGAQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEHRERSLOTLRDIORMLFPDEKEFTGAQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2001US-0328944P.
; 2001US-0345384P.
; 2001US-0343880P.
; 2001US-0345143P.
; 2001US-0332430P.
                                                                                                       fumigatus
                                                                                                                                                                                                                                    fumigatus essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.6%;
                                                                                                                                                        essential gene; Aspergillus fumigatus; biofilm; antibody; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection and treatment, disorders, e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                      #511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,,</u>
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                                                                                                                                                                                infection;
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ABJ26453
ID ABJ26453
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KW Fungi
KW Fungi
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                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC organism such as A. fumigatus, to treat a non-infectious disease in a CC subject (e.g. cancer), to prevent or inhibit formation on a surface of a by A. fumigatus, or to prevent or inhibit formation on a surface of a CC biofilm comprising A. fumigatus. The polynucleotides are useful for CC therapeutic use, as markers for host tissues in which the pathogenic CC organisms invade or reside, for comparing with the DNA sequence of A. CC fumigatus to identify duplicated genes or paralogues having the same or CC similar biochemical activity and/or function, for comparing with DNA CC sequences of other related or distant pathogenic organisms to identify sequences of other related or distant pathogenic organisms to identify contained or thologous essential or virulence genes, for selecting and CC making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an CC antigen to raise anti-DNA antibodies or to elicit another immune CC response, and for identifying polynucleotides encoding the other protein which binding occurs or to identify inhibitors of the binding CC interaction. The polypeptides may be used to raise antibodies or to elicit immune levels of the polypeptides may be used to raise antibodies or to clicit immune levels of the potropin in biological fluids, as a marker for host tissues in which bathogenic organism invade or reside
                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids the invention are used to treat or prevent infections by a pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-2001;
27-APR-2001;
                                      Fungicide; cytostatic;
cancer; contamination;
                                                                                                                                                                            ABJ26453
                                                                                                                                                                                                              ABJ26453 standard; protein; 618 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 603
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09-JUL-2001;
  Aspergillus fumigatus
                                                                                                 Aspergillus
                                                                                                                                       16-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nost tissues in which pathogenic organism invade or reside, and t
solate correlative receptors or ligands in the case or virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                    DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a protein of one of the essential genes yillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                              DGVETEKIREKD---EVEKKLERMLFGDDEGFVGA
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                               fumigatus essential gene protein #1111.
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2001US-0303899P.
2001US-0316362P.
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2001US-0287066P.
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                                                                                                                                                                                                                                                                                                                                                                                                             31.4%; Score 57.5;
31.4%; Pred. No. 41;
                                    essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
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                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                               6,
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                                                                                                                                                                                                                                                                                                                                                                        CC therapeutic use, as markers for host tissues in which the pathogenic corpanisms invade or reside, for comparing with the DNA sequence of A. CC fumigatus to identify duplicated genes or paralogues having the same or cc similar blochemical activity and/or function, for comparing with DNA cc potential orthologous essential or virulence genes, for selecting and cc making oligomers for attachment to a nucleic acid array for examination cf expression patterns, for raising anti-protein antibodies, as an cc antigen to raise anti-DNA antibodies or to elicit another immune cc with which binding occurs or to identify inhibitors of the binding cc interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for comparine levels of the protein in biological fluids, as a marker for const tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence cf factors. This sequence represents a protein of one of the essential genes or vo
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the architecture.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 618 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295890P.
09-UUL-2001; 2001US-0303899P.
                                                                                                                            ABU44941 standard; protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention are used to treat or prevent infections by a pathog organism such as A. fumigatus, to treat a non-infectious disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-2001; 2001US-0316362P
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                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                           1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                        DGVETEKIREKD---EVEKKLERMLFGDDEGFVGA
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                31.4%;
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                                                                                                                                                                                                                                                                                                                Score 57.5;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                           35
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                                                                                                                                                                                                                                                                                                                                   Length 618;
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                                                                                                                                                                                                                                                                                              Сарв
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Protein encoded by Prokaryotic essential gene #30468.

19-JUN-2003 (first entry)

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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

((1) a vector comprising a promoter operably linked to the nucleic acid cenoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the cantisense expression is inhibited by the concleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular consolidation or the activity of agene in an operon required for proliferation or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (7) identifying a compound that influences the activity of the gene product to that has an activity against a biological pathway crequired for proliferation, or that inhibits proliferation or the biological pathway in which acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the conditions or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational conditions or screening for homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, creaming activity of sevening homologous nucleic acids of the target prokaryotic essential genes. Note: The sequence data for this gratent did did not format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                               Sequence 411
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                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-029926/02
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                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated nucleic acid comprising any one 6213 antisense sequences given in the specification where express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ġ ſ
                                                                      l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                candidate molecules
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LSQEQUEHRERSLOTLRDIQRMLFPDEK 30
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 72865; 1766pp; English
                                                                      Conservative
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2001US-0342923P.
2002US-00072851.
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Carr G
                                                                                              31.1%;
                                                                                                                                                                                                                                                  _pct_sequences
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ရီ (
                                                               Score 57; DB Pred. No. 31; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for rational drug discovery programs
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                                                                                                                               6;
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Forsyth
                                                                                                                               Length 411;
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Xu HH;
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RESULT 24
ABU47461
ABU47461
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ABU477461
ACC ABU47
                                                                                CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated concleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding contisense nucleic acid; (4) an antibody capable of specifically binding che polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for crequired for proliferation, (7) identifying a compound that influences the activity of crequired for proliferation, or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which he test compound that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a cc compound is activity; (11) a culture comprising strains in which the gene cc product is overexpressed or underexpressed; (12) determining the extent compound is activity; (13) a culture comprising strains in which the gene cc identifying proteins or screening for homologous nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the catent of compound proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational crequired for proliferation in cells other than S. aureus, S. typhimurium, c. patent did not form part of the printed specification, but was obtained concluded to compound that inhibits the concluded provided by one of the target provide essential genes. Note: The sequence data for this concluded in electronic format directly from WIPO at
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06-SEP-2001; 2
25-OCT-2001; 2
08-FEB-2002; 3
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 75385; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELITRA PHARM INC.
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Trawick
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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Carr G
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Forsyth
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                                                                                                                                                      Query Match
Best Local :
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            This invention relates to novel genes and the encoded proteins thereof that are derived from the sea squirt Ciona intestinalis. Specifically, it refers to those genes that are expressed in the tissues or organs of the sea squirt during its developmental phase. The present invention of the mechanism of development and hence for developing regeneration medicines and gene therapy techniques. Accordingly, they can be used in the research of various genetic diseases, as well as the analysis of cell proliferation, differentiation and reproduction. Furthermore, such compositions can be useful for environmental measurements and water surveys, particularly for sea water surveys, and also for the preparation of transformed sea squirt for improving edibility of sea squirt such as Halocynthia roreti. This polypeptide sequence is a sea squirt protein sequence that has tissue specific expression during development, given in
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 248; 1846pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mechanism of development of tissue or organ of sea squirt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sea squirt; regeneration medicine; gene therapy; cell proliferation;
differentiation; reproduction; environmental measurement; water survey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sea squirt protein with tissue specific expression in development Seq248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                               exemplification of the invention.
391 MAQEEILRKERELQSARQKLAQIRRMRYKDDSE 423
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                                                              LSQEQLEHRERSLQTLR----DIQRMLFPDEKE 31
                                                                                                                            Conservative
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; Pred. No. 86;
6; Mismatches
                                                                                                                     Score 56; DB (
Pred. No. 44;
9; Mismatches
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RESULT 26 ABR53351

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RESULT 27
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
                                            protein complex;
                                                                       Disease treating protein complex-derived protein
                                                                                                      06-MAY-2004
                                                                                                                                                             ADK63408 standard; protein; 584 AA
                                                                                                                                                                                                                                                                                                                                                               Sequence 584 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 1567; 17pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACC61393.
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SREEIEIRNQTISTIREAVKQLWPD
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M, Schultz JD, Superti-Furga GD;
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                                                                                                      (first entry
                                            drug target; diagnosis
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                  Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
  Bacteria
                                                                                                                                                                                                                                                                                         Bacterial polypeptide #2015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN19362 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cond protein, or its derivative, fragment, homologue or variant oteins are selected from given protein complexes, which are not the specification. The variants are encoded by nucleic acids the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to novel protein complexes comprising a first and protein, or its derivative, fragment, homologue or variant.
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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cc transformed plant having an improved property. The plant is a crop plant cc such as maize or soybean. The method of producing a transformed plant cc such as maize or soybean. The method of producing a transformed plant cc recombinant DNA construct and growing the transforming a plant with the cc polynucleotide or polypeptide is useful for improving plant properties. Cc improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, collerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of carbohydrate, nitrogen or condition, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan cc production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not compare the pathon of the printed specification but was obtained in electronic compared them to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the condition of the printed specification but was obtained in electronic compared to the condition of the printed specification but was obtained in electronic compared to the condition of 
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hyperthermophile;
protein activity of
                                                           Hyperthermophile Methanopyrus kandleri protein #835.
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(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                                                                                                                                                                                                                                                       4 SQEQUEHRERSLQTLRDIQRMLFPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                 Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HINKLE G
SLATER S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAO Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHEN X
                                                                                                                                                                                        standard; protein; 818
                                                                                                                                                                                                                                                                                                SREEIEIRNOTISTIREAVKOLWPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                     (first entry)
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protein stability enhancement;
enhancement.
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                                                                                                                                                                                                                                                                                                                                                                                                       36.6%;
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                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB
Pred. No. 63;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen
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63;
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                                                                                                                                                                                                                                                                                                                                                                                    6,
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RESULT 30
ADL83239
ID ADL83239
XX ADL83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises the amino acid sequence of proteins from the hyperthermophile Methanopyrus Kandleri, the invention also comprises the complete genome from Methanopyrus kandleri. The Methanopyrus kandleri proteins of the invention are useful for enhancing the stability and/or activity of other proteins. The Methanopyrus Kandleri genome is useful is variety of diagnostic and analytical methods. The present amino acid sequence represents a Methanopyrus kandleri protein of the invention.
                                                                                                                                                                                                                                                                                                                                                      Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic; Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FIDE-)
(MALY/)
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14-MAY-2002; 2002US-0380423P.
16-SEP-2002; 2002US-0410974P.
                                                                                                                                                                                                                                  WO2004024097-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO84721, SEQ ID 441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADL83239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL83239 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kandleri proteins, and the encoded proteins, useful as a medicaments or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acids encoding any of about 1700 Methanopyrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                           16-SEP-2002; 2002US-0411392P
                                                                                                                              15-SEP-2003;
                                                                                                                                                                                                                                                                                                                                      immune-mediated inflammatory disease;
                        (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIDELITY SYSTEMS INC. MALYKH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM27081.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 835; 1023pp; English.
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                                                                                                                              2003WO-US029097.
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4; Mismatches
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RESULT 31
ADQ17519
ID ADQ17
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Best Local :
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Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or antylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgM deficiency, selective IgM subclasses, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                  Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1132 AA;
                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-2002; 2002US-0429739P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soft tissue sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human soft tissue sarcoma-upregulated protein - SEQ ID 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ17519 standard; protein; 1132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and screening of therapeutically useful reagents.
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                                                                                                                                                                                      WPI; 2004-441208/41.
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                                                                                                                                                                                                                                                                                                                       PROTEIN DESIGN LABS INC.
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                                                                                                                                                                                                                                                   Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENORSHOELISQLLOSYMKLLLPDDEKFHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.6%;
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                                                                                                                                                                                                                                                      Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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Pred. No. 1.3e+02;
8; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schoenfeld JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619
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RESULT 32
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                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABIJ0511), expressed DNA sequences (ABLIG175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the ABB72072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
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8; Mismatches
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                                                                                                                      the 6213 antisense sequences given in the specification where expression (C) of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense cancel cacid; (2) a host cell containing the vector; (3) an isolated complete acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the containing the vector; (3) an isolated complete cacid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for complete                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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06-SEP-2001; 2
25-OCT-2001; 2
08-FEB-2002; 2
organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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late candidate molecules f
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Pred. No. 1
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New breast specific nucleic acid molecules and polypeptides useful for diagnosing, preventing or treating breast cancer, for producing transgenic animals or cells, or for research purposes.
                                                                                                                                  The invention relates to a novel isolated breast specific nucleic acid (BSNA) molecule which comprises a nucleic acid sequence encoding any of the 107 breast specific protein (BSP) amino acid sequences fully define in the specification. The molecules of the invention demonstrate cytostatic activity and may be useful for diagnosing, preventing or treating breast cancer, possibly via vaccine production or gene therapy The current sequence is that of a human breast cancer-related protein of the current sequence is that of a human breast cancer-related protein of the current sequence is that of a human breast cancer related protein of the current sequence is that of a human breast cancer related protein of the current sequence is that of a human breast cancer related protein of the current sequence is that of a human breast cancer related protein of the current sequence is that of a human breast cancer related protein of the current sequence is that of a human breast cancer related protein of the current sequence is that of a human breast cancer related protein of the current sequence is that of a human breast cancer related protein of the current sequence is that of a human breast cancer related protein of the current sequence is the current sequence is that of a human breast cancer related protein of the current sequence is the cu
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         Sequence 237
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Pred. No. 98;
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Human protein sequence SEQ ID NO:16943
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                                                                                                                                                        AAB95073 standard; protein; 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 248;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 37
ABR82444
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                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 complementary strand of a polynucleotide which comprises one of the 5602 complementary strand of a polynucleotide; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a sequence complementary to a complementary strand of a polynucleotide which comprises a comprising a sequence complementary to a polynucleotide which comprises a s'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense threspy and in comprise to the secification. The primers are useful for synthesising polynucleotides, company the primers are useful for synthesising polynucleotides, company the primers are useful for synthesising polynucleotides, company the primers and so useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and any specialised methods. AAH03166 to AAH13628 and company to the full-length compan
                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 12
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Ishii S,
                        06-NOV-2003
                                                                                                            ABR82444 standard;
                                                                   ABR82444;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1999; 99UP-00300253.
11-JAN-2000; 2000UP-00118776.
02-MAY-2000; 2000UP-00183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                                                                                                                                                                                Similarity
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                      GLRTEGLFRRSASVQTVREIQRL 246
                                                                                                                                                                                                                                                               GLSQEQLEHRERSLOTLRDIQRM 24
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                        (first entry)
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                                                                                                          protein;
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                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                              Score 55; DB
Pred. No. 41;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                     DB 4;
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Ctsuki
                                                                                                                                                                                                                                                                                                                                                  Length 294;
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RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate neoplastic condition. The method involves (a) contacting a specimen from the individual with an androgen responsive prostate specific (ARP)15 binding agent that selectively binds an ARP15 polypeptide; (b) determining a test expression level of ARP15 polypeptide in the specimen; and (c) comparing the test expression level to a non-neoplastic control expression level of ARP15 polypeptide, where an altered test expression level as compared to the control expression level indicates the presence of a prostate neoplastic condition in the susceptibility to a prostate neoplastic condition or for treating or reducing severity of a prostate neoplastic condition. The present sequence represents a human ARP13 polypeptide
                                                                                                                                                                                                                                    Human; androgen responsive prostate specific polypeptide; ARP; prostate neoplastic condition; prostate cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                             Human androgen responsive prostate
                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ74859 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing or predicting susceptibility to a prostate neoplastic condition by contacting a specimen from the individual with an ARP15
                                                          15-JUL-2004
                                                                                                                     US2004137440-A1
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 78; Page 195-197; 227pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding agent that selectively binds an
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12; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.1%;
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15-JAN-2003; 2003US-00345837

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTPase-activating protein; GTPAP; cell signalling; cell proliferative disorder; colon cancer; immune human; Rho GTPase activating protein 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or reducing the severity of a prostate neoplastic condition in an individual. The polymucleotides, polypeptides and methods of the invention are useful for diagnosing and treating prostate cancer. sequence represents a human ARP polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human androgen responsive prostate specific (ARP) polynuclectides and the polypeptides they encode. The invention also relates to a method of diagnosing or predicting susceptibility to prostate neoplastic condition in an individual and a method for treating prostate neoplastic condition in an individual and a method for treating prostate neoplastic condition in an individual and a method for treating prostate neoplastic condition in an individual and a method for treating prostate neoplastic condition in an individual and a method for treating prostate neoplastic condition in an individual and a method for treating prostate neoplastic condition in an individual and a method for treating prostate prostate specific condition in an individual and a method for treating prostate prostate specific condition in an individual and a method for treating prostate prostate prostate specific condition in an individual and a method for treating prostate prost
                                    New GTPase-activating proteins designated GTPAP-1 and its variant GT are useful to diagnose, stage, treat and monitor cell signaling and proliferative disorders, particularly colon cancer.
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N-PSDB; ADQ74858.
                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-2000; 2000US-00507765
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12; Conservative
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                                                                                                                                                                                                                                                                                                                                                    INCYTE GENOMICS INC.
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176. .189
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                                                                                                                                                                                            (BSNA) molecule which comprises a nucleic acid sequence encoding any of the 107 breast specific protein (BSP) amino acid sequences fully defined in the specification. The molecules of the invention demonstrate cytostatic activity and may be useful for diagnosing, preventing or treating breast cancer, possibly via vaccine production or gene therapy. The current sequence is that of a human breast cancer-related protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               their encoding cDNAs. The protein is used to diagnose, stage, treat monitor cell signalling, immune and cell proliferative disorders, particularly colon cancer. The present sequence is human Rho GTPase activating protein 8 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New breast specific nucleic acid molecules and polypeptides useful diagnosing, preventing or treating breast cancer, for producing transgenic animals or cells, or for research purposes.
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05-DEC-2002;
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                                                                                                                 Sequence 337 AA;
                                                                                                                                                                      The current sequence the invention.
                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated breast specific nucleic acid
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(c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Disclosure; SEQ ID NO 3; 62pp; English.

The invention relates to a polypeptide sharing one or more homologous amino acid domains with a Legless (Lgs) protein and is therefore a functional homologue of Lgs. The invention also relates to a nucleotide sequence encoding a protein present in invertebrate and/or vertebrate organisms, the nucleotide sequence encoding a protein comprising a positive function in a regulatory pathway and the use of the polypeptide for the isolation of Lgs-binding proteins by carrying out an assay chosen from an in vitro binding assay with such a peptide or a co-immunoprecipitation from vertebrate or invertebrate cell lysates or a mammalian or yeast two hybrid assay. The polypeptide and polynucleotide

PT Legless pro	WPI;	PI Basler XX	PA (UYZU-)	PR 28-JUL-: PR 27-JUL-:	PF 22-SE	PD 26-FEB-		Homo	Human; cell pi breast; tissue	Human	20-MA	ADJ71891;	RESULT 1 ADJ71891 ID ADJ71891		44	43	42	4 4	39	38 ·	7 G	35	س در س 4	32	ω <u>,</u>	30	28	27	26	
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logue of Legless, use		Kramps T, Peter O;							cell differentiation disorder; sorder; cancer; Wnt pathway; medulloblastoma; rain; thyroid; skin; blood dieease; tissue repair; cytostatic; Lgs/Bc19.					ALIGNMENTS					Abj26489							Abm80775		Aae15	Abq15	
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which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regeneration and
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                                                                                                                                                                                                                                                                                                                                                                           invention relates to a novel method for detecting soft tissue sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ginsburg WM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 1764; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repair. This sequence represents a human Lgs/Bc19 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zlotník A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 5.2e-14;
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Best Local
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                                                                       This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be use to promote tissue regeneration and repair. This sequence represents the human legless (1gs) protein homologue 1gs/bc19 described in the
  Sequence 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptide useful in therapeutic cell fate such as cell differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF88467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Legless; human; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; closm; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Example II; Fig 8B; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Basler K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000; 2000US-0221502P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRUNNER E.
) FROESCH B.
) KRAMPS T.
) PETER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brunner E,
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Pred. No. 5.5e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating disorders proliferation.
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Query Match Best Local

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                                                                                                                                                                                       Matches
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Best Local :
                                                                                                                                                                                                                                                                                                           The invention relates to novel legless (1gs) proteins and polynucleotides encoding such proteins. Igs sequences are useful for the treatment of disorders of cell fate such as differentiation or proliferation. The invention is used to treat blood disease or a cancerous condition characterised by over-stimulation of the Wnt pathway such as colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer and is administered to prevent progression from a pre-neoplastic or non-malignant condition to a neoplastic or malignant state. It is administered to promote tissue regeneration and repair. The invention is also useful in the therapy of diseases cost by an over-activation of Wg pathway. It is useful for reducing 1gs gene expression in an invertebrate or vertebrate organism or an invertebrate or vertebrate cell line. The invention is also useful in gene therapy. The present sequence is human log/bc1e protein useful in the invention.
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                   ADJ70152 standard; protein; 1426
                                                                                                                                                                                                                                                              Sequence 1426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 8B; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Lgs polypeptide useful diagnosing disorders of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Basler K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000;
27-JUL-2001;
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                                                                                                                                  1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
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                                                                                                                                                                                                                                                                                                   protein used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                       Conservative
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2001US-00915543.
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                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                   in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Froesch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for isolation of Lgs-binding fate, treating diseases such
                                                                                                                                                                                 Score 136; DB /;
Pred. No. 5.7e-12;
***-matches 0;
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                                                                                                                                                                                                                       Length 1426;
                                                                                                                                                                                       Indels
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17-JUN-2002;
20-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                 This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoolonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                           Sequence 1426
                                                                                                                                                                                                                                                                 anticonvulsant, antiarthritic, osteopathic, ophtle cytostatic activities. This polypeptide sequence mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huntington's disease;
                                                                                                                                                                                                                                                                                                                       compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-2003; 2003WO-US010870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteopathic; ophthalmological; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human heat mitochondrial protein as a therapeutic target SeqID1958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-2004
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177
                                                                                                   28;
                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease.
                         VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
VYVFSTEMANKAAEAVLKGQVETIVSFH 204
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                                                                                                   100.0%;
llarity 100.0%;
Conservative C
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2002US-0389987P
2002US-0412418P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Β,
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                                                                                                                            Score 136; DB 7
Pred. No. 5.7e-1
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                                                                                                   Mismatches
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                                                                                                                                                     Length 1426;
                                                                                                                                                                                                                                                                                             is a human heart
                                                                                                        Indels
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standard;

protein; 1426 AA.

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                                                                 Sequence 1426 AA;
                                                                                                                                                                                                                                                                                                                         Novel polypeptide sharing one or more homologue amino acid domains Legless protein being functional homologue of Legless, useful for diagnosing disorders of cell fate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; legless; lgs; cell differentiation disorder; cell proliferation disorder; cancer; wnt pathway; medulloblastoma; colon; breast; head; neck; brain; thyroid; skin; blood disease; tissue regeneration; tissue repair; cytostatic; Lgs/Bc19.
                                                                                 polypeptide
                                                                                                                                                                                                                                                                      The invention relates to a polypeptide sharing one or more homologous amino acid domains with a Legless (Lgs) protein and is therefore a functional homologue of Lgs. The invention also relates to a nucleotide
                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                   Basler K,
                                                                                                                                                                                                                                                                                                                                                                                                   (UYZU-) UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000;
27-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-2003; 2003US-00664859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004038901-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Lgs/Bc19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-2004 (first entry)
177
                                                                                                                                                                                                                                                                                                                                                                  2004-203288/19
                                 28;
                                        Similarity
                                                                                                                                                                                                                                                                                                       2; SEQ ID NO 15; 62pp; English
           VYVFSTEMANKAAEAVLKGQVETIVSFH 28
VYVFSTEMANKAAEAVLKGQVETIVSFH 204
                                                                                                                                                                                                                                                                                                                                                                                 Brunner E,
                                                                                  of the invention.
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-00915543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide
                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                  Froesch
                                                                                                                                                                                                                                                                                      a polypeptide sharing
                                0;
                              Score 136; DB 8;
Pred. No. 5.7e-12;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                 Kramps
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                                               Length 1426;
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bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human BCL9 homologue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haematopoiesis regulation; tissue growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB11808 standard; peptide; 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO:2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunomodulator;
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activin;

05-FEB-2001; 2001WO-US003800

03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875.

Ľ, Ç Drmanac

WPI; 2001-457740/49.

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis

Claim 20; Page 256-257; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and convention also relates to vectors and recombinant host cells comprising a conclusive fine the invention, methods of producing the novel polypeptides, and the polypeptides of the invention, methods of detecting the nucleotides of producing the novel polypeptides, and methods of identifying compounds which convergence in a sample, and methods of identifying compounds which convergence in the polypeptides, methods of identifying compounds which convergence in the polypeptides of the invention and methods of identifying compounds which convergence in the polypeptides of the invention may of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differential therapeutic applications. The polypeptides of the invention or cell differential therapeutic; probable biological activity; in the invention or cell differential therapeutic; activity; tissue growth activities; chemotactic or chemotheric activities; activities; haemostatic, thrombotic or thrombotic or thromboty activity; activity tissue growth activities; or may be conditions on their biological activities, haemostatic, thrombotic or involved in oncogenesis, cancer cell proliferation or metastasis.

Compending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions medical conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions and decrease, conditions and uncers), and abnormal conditions (e.g., of burns, incisions and ulcers), while those with

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the encoded proteins (AAO00010-ÅAO13910) that exhibit activity elating to tytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 19747; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2001
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polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to human polynucleotides (AAI79941-AAI93841)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ytokine; cell proliferation; cell differentiation; gene therapy;
peptide therapy; stem cell growth factor; haematopoiesis;
rowth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYVFSTEMANKAAEAVLKGQVETIVSFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             techniques. The pr
de of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor; immunomodulatory; cancer; rendisorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 19747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 5.7e-12;
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Query Match Best Local S Matches 16

l Similarity

72.1%; ilarity 57.1%; Conservative

9

Score 98; DB 7; Pred. No. 4.9e-08; 9; Mismatches 3

Length 28;

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Gaps

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VYVFSTEMANKAAEAVLKGQVETIVSFH

28

IFVFSTQLANKGAESVLSGQFQTIIAYH

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RESULT 9
ABMO1528
ABMO1528
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Best Local Similarity
                                                  The invention relates to novel legless (1gs) proteins and polynucleotides encoding such proteins. Igs sequences are useful for the treatment of disorders of cell fate such as differentiation or proliferation. The invention is used to treat blood disease or a cancerous condition characterised by over-stimulation of the Wnt pathway such as colon, breast, head and neck, brain, thyroid, medulloblastcma or skin cancer and is administered to prevent progression from a pre-neoplastic or non-malignant condition to a neoplastic or malignant state. It is administered to promote tissue regeneration and repair. The invention is also useful in the therapy of disease cost by an over-activation of Wg pathway. It is useful for reducing 1gs gene expression in an invertebrate or vertebrate organism or an invertebrate or vertebrate cell line. The invention is also useful in gene therapy. The present sequence is prosophila species legless (1gs) peptide
      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Lgs polypeptide useful diagnosing disorders of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Legless protein; lgs; cell fate disorder; blood disease; gene therapy; cancer; tissue regeneration; tissue repair; cytostatic.
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27-JUL-2001; 2001US-00915543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 28; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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      AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7B; Opp; English
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Pred. No. 4.5e-12;
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RESULT 10
ADJ71890
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                                                                                                                                              The invention relates to a polypeptide sharing one or more homologous CC amino acid domains with a Legless (Lgs) protein and is therefore a CC functional homologue of Lgs. The invention also relates to a nucleotide condition of Lgs. The invention also relates to a nucleotide cC sequence encoding a protein present in invertebrate and/or vertebrate according a protein of Lgs-binding proteins by carrying out an assay chosen cC for the isolation of Lgs-binding proteins by carrying out an assay chosen cC immunoprecipitation from vertebrate or invertebrate cell lysates or a cc mammalian or yeast two hybrid assay. The polypeptide and polynucleotide care useful for treating disorders of cell fate, which involves carrying related to treating disorders of cell fate, which involves care useful for treating disorders of cell fate, which involves care useful for treating and natural compounds being capable of cragments, lgs antisense DNA, lgs antisense RNA, lgs double-stranded RNA, carrying with Lgs function, synthesis and degradation. The disorders care related to treat a cancerous condition by preventing progression from a pre-neoplastic or non-malignant condition to a neoplastic or cancerous to the Wnt pathway and is medulloblastoma or cancer of the compound may also be administered to brain, thyroid or skin. The therapeutic compound may also be administered to a concer of the compound is medulloblastoma or cancer of the compound may also be administered to a procential to a promote tissue
                                                                      Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptide sharing one or more homologue amino acid domains with Legless protein being functional homologue of Legless, useful for diagnosing disorders of cell fate.
                                                                                                                                            Sequence 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 2; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fruit fly; legless; lgs; cell differentiation disorder; cell proliferation disorder; cancer; Wnt pathway; medulloblastoma; colon; breast; head; neck; brain; thyroid; skin; blood disease;
                                                                                                                                                                                regeneration and repair. This sequence represents a Drosophila peptide fragment of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Basler K,
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27-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fruit fly legless (lgs) peptide fragment #1
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                                                                          16;
                                                                                         Similarity
                    VYVFSTEMANKAAEAVLKGQVETIVSFH 28
IFVFSTQLANKGAESVLSGQFQTIIAYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunner E,
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                                                                        Conservative
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2001US-00915543.
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                                                                                       72.1%;
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                                                                  Score 98; DB 8
Pred. No. 4.9e
9; Mismatches
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 28
                                                                                         4.9e-08
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                                                                                                        Length 28;
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RESULT 11
ABBSULT 12
ABBSE 779
ID ABBSE XX
AC ABBSE XX
AC ABBSE XX
AC ABSSE XX
AC ABSSE XX
AC ABSSE XX
DTOSC XX
PR 23-MJ
PR 11-JI
XX
PR 11-JI
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PR 23-MJ
PR 11-JI
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PR 11-JI
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PR 11-JI
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DR N-PSI
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AAB71228
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL18176-ABL30511), expressed DNA sequences (ABL0840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                       D. melanogaster lgs protein.
                                                                                                                                                                                                                                                                          AAB71228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes from Drosophila and interactions.
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Legless; fruitfly; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon;
                                                                                                                                                       18-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 3129; 21pp + Sequence Listing; English
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                           323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                       standard; protein; 1464
                                                                                                                                                                                                                                                                                                                                                                                                                        IFVFSTQLANKGAESVLSGQFQTIIAYH 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.1%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 98; DB
Pred. No. 5.4e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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RESULT 13
ABW01527
ID ABW01527
ID ABW01527
ID ABW01527
AC ABW01
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AC ABW01
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 16
                                                                                             Legless cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain,
                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruitfly) legless disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                               where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the Drosophila melanogaster (fruitfly) legless (lgs) protein described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel
cell:
                                                                                                                                    Drosophila species legless
                                                                                                                                                                                             ABW01527
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
              19-JUN-2003.
                                        US2003114413-A1
                                                                 Drosophila sp.
                                                                                                                                                                   15-JAN-2004
                                                                                                                                                                                                                        ABW01527 standard; protein; 1464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example II; Fig 2; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-635689/68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000US-0221502P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-2001; 2001US-00915543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002086986-A1
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                                                                                                                                                                                                                                                                                                                                                     16;
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BRUNNER E.
FROESCH B.
                                                                                             protein;
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                                                                                                                                                                                                                                                                                           ::||||::|| ||:|| || :||:::|
IFVFSTQLANKGAESVLSGQFQTIIAYH 345
                                                                                                                                                                                                                                                                                                                       VYVFSTEMANKAAEAVLKGQVETIVSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunner E,
                                                                                                                                                                                                                                                                                                                                                   72.1%;
ilarity 57.1%;
Conservative
                                                                                                                                                                  (first entry)
                                                                                      n; 198; cell fate disorder; blood disease; regeneration; tissue repair; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :
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                                                                                                                                      (lgs) protein
                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                   Score 98; DB
Pred. No. 5.5e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kramps T,
                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                   ; DB 5;
. 5.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                              Length 1464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating disorders of proliferation.
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                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents the described in the
                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                          therapy;
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-829432/
N-PSDB; AAD62641.
                                                                                                                                                                                                                                 Fruit fly; legless; lgs; cell differentiation disorder; cell proliferation disorder; cancer; Wnt pathway; medulloblastoma; colon; breast; head; neck; brain; thyroid; skin; blood disease;
                                                                                                                                                                                                                                                                                                                                                                           ADJ71911
                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                         Fruit fly legless (lgs) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Lgs polypeptide useful diagnosing disorders of cell
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27-JUL-2001;
              Basler K,
                                                                  28-JUL-2000;
27-JUL-2001;
                                                                                                          22-SEP-2003; 2003US-00664859
                                                                                                                                        26-FEB-2004.
                                                                                                                                                                                                                      tissue regeneration; tissue repair; cytostatic.
                                                                                                                                                                                                                                                                                                                     20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Fig 2; Opp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-2002; 2002US-00322579
                                         (UYZU-) UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-829432/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                              318 IFVFSTQLANKGAESVLSGQPQTIIAYH 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                           standard; protein; 1464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunner E,
              Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0221502P.
2001US-00915543.
                                                                  2000US-0221502P
2001US-00915543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.1%;
              Froesch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Froesch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98; I
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for isolation of Lgs-binding proteins, fate, treating diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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              Kramps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ή
               Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1464;
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RESULT 15
AAU78460
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC organisms, the nucleotide sequence encoding a protein comprising a
CC positive function in a regulatory pathway and the use of the polypeptide
CC for the isolation of Lgs-binding proteins by carrying out an assay chosen
CC immunoprecipitation from vertebrate or invertebrate call lysates or a
CC mammalian or yeast two hybrid assay. The polypeptide and polynucleotide
CC are useful for treating disorders of cell fate, which involves
CC administering therapeutic compounds chosen from invertebrate and
CC vertebrate Lgs protein homologues or fragments, antibodies, antibody
CC fragments, lgs antisense DNA, lgs antisense RNA, lgs double-stranded RNA,
CC small peptides or chemical and natural compounds being capable of
CC interfering with Lgs function, synthesis and degradation. The disorders
CC are related to cell differentiation or cell proliferation. The compound
CC is administered to treat a cancerous condition by preventing progression
CC from a pre-neoplastic or non-malignant condition by preventing progression
CC malignant state. The cancerous condition is characterised by over-
CC stimulation of the Wnt pathway and is medulloblastoma or cancer of the
CC colon, breast, head and neck, brain, thyroid or skin. The therapeutic
CC regeneration and repair. This sequence represents the Drosophila Lgs
CC conformation of the first in the compound of the compound condition of the worth of the compound of the compound condition condition of the compound condition condit
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Best Local S
Matches 16
                                                                                                                                                                                                   28-MAR-2002.
                    Akiyama
                                                                                                         22-SEP-2000; 2000JP-00287876
                                                                                                                                                   19-SEP-2001; 2001WO-JP008140
                                                                                                                                                                                                                                          WO200224738-A1
                                                                                                                                                                                                                                                                                                                                  expressed
                                                                                                                                                                                                                                                                                                                                                                                                Mouse beta-catenin nuclear localised protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU78460 standard; protein; 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptide sharing one or more homologue amino acid domains with Legless protein being functional homologue of Legless, useful for diagnosing disorders of cell fate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                              (KYOW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence encoding a protein present in invertebrate and/or vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a polypeptide sharing one or more homologous amino acid domains with a Legless (Lgs) protein and is therefore a functional homologue of Lgs. The invention also relates to a nucleotide
                                                                                                                                                                                                                                                                                        musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318
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                                                                                                                                                                                                                                                                                                                                                      beta-catenin nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                              куома накко кодуо кк
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                                                                                                                                                                                                                                                                                                                               sequence tag
                    Adachi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                  localised protein;
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Pred. No. 5.5e-06;
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                                                                                                                                                                                                                                                                                                                                                    cancer;
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RESULT 16
ABP06595
ID ABP06
XX ABP066
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a beta-catenin nuclear localised protein and DNJ encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear
The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Tab in the specification). ABN15762 to ABN27252 encode the human ORFX
                                                                                                                                                                 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperproliferative disorder; psoriasis; benign tumour; haemorrhage degenerative disorder; osteoarthritis; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; gene therapy; cancer; hyperproliferative disorder; psoriasis; benign tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New beta-catenin nuclear localized protein for diagnosis and treatment of diseases associated with nuclear localization of beta-catenin e.g.
                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                               Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200192523-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP06595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP06595 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myasthenia gravis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           localised protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                           2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 VYVFTTHLANTAAEAVLQGRAESILAYH 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \vdash
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         CURAGEN CORP.
                                                                                                                                                                                                                                                                                    ABN22347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYVFSTEMANKAABAVLKGQVETIVSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.1%;
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                                                                                                          13172; 1037pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:13172.
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Pred. No. 2.4e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .4e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cirrhosis;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2002
                                                                                                                                           diseases
                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                WPI; 2002-330014/36
                                                                                                                                                                                                                                                  Akiyama
                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200224738-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; beta-catenin nuclear localised protein; cancer; gene therapy; EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse beta-catenin nuclear localised protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU78461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU78461 standard; protein; 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114 AA;
                                                                                                                                       New beta-catenin nuclear localized protein for diagnosis and treatment diseases associated with nuclear localization of beta-catenin e.g.
                                                                                                                                                                                                                                                                                     (KYOW)
                                                                                                                                                                                                                                                                                                                     22-SEP-2000; 2000JP-00287876
                                                                                                                                                                                                                                                                                                                                                        19-SEP-2001; 2001WO-JP008140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                   куома накко косуо кк
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                                                                                                                                                                                              ABK47632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYVFSTEMANKAAEAVLKGQVĖTIVSFH 28
||||:|:||||||||:|:::|:::|
VYVFTTHLANTAAEAVLQGRADSILAYH 105
                                                                                                                                                                                                                                                  Adachi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
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The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence

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MANKAAEAVLKGQVETIVSF 27

l Similarity 15; Conserv

Conservative

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Indels

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Claim 2;

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91-92; 113pp; Japanese

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Query Match
Best Local S
Matches 15
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Best Local
                                                                                  production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiseis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represents the amino acid sequence of mouse beta-catenin nuclear localised protein #2
                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haemato tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO07544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001
                                                           Sequence
                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 21436; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                             and treating e.g. leukemia,
                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                           2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LANTAAEAVLQGRAESILAYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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               47.8%;
75.0%;
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Score 65; DB
Pred. No. 0.04
1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell differentiation; gene therapy;
                 DB 4;
0.041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
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                             Length 113
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ADMUSITION 19
ADMUSITION 10
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                                                                                                                                                                         Matches
                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                             Sequence 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel method for targeting disruption of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; SEQ ID NO 1988; 598pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-2002; 2002JP-00319011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene disruption;
                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermococcus kodakaraensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN48110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN48110 standard; protein; 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nomologous recombination; hyperthermostable archaebacterium;
        69
                                                                                3 VFSTEMANKAAEAVLKGQVETIVS 26
                                                                                                                                                                    Similarity
9; Conserv
IYALKKNNKAPKAIIVGEAETIVA
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                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                      39.0%;
                                                                                                                                                                    9;
                                                                                                                                                                                                      Score 53; 1
Pred. No. 3
                                                                                                                                                            core 53; DB 8; red. No. 3.8; Mismatches
    92
                                                                                                                                                                6
                                                                                                                                                                                                                                        Length 133;
                                                                                                                                                                    Indels
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RESULT 20

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RESULT 21
AAG33446
ID AAG33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                     EP1033405-A2
                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                              Zea mays protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG33446 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                 termination sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABD00263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebsiella pneumoniae protein; antibacterial; Vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                          mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 LYRQDLAPEAAEAVLHGKWDTQASMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No.
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18-JUN-1999; 99US-01 21-JUN-1999; 99US-01 22-JUN-1999; 99US-01 23-JUN-1999; 99US-01 23-JUN-1999; 99US-01 24-JUN-1999; 99US-01 24-JUN-1999; 99US-01 30-JUN-1999; 99US-01 30-JUN-1999; 99US-01 01-JUL-1999; 99US-01 01-JUL-1999; 99US-01 01-JUL-1999; 99US-01 02-JUL-1999; 99US-01 08-JUL-1999; 99US-01 08-JUL-1999; 99US-01	04-JUN-1999; 99US-01. 07-JUN-1999; 99US-01. 10-JUN-1999; 99US-01. 11-JUN-1999; 99US-01.	PR 04-MAY-1999; 99US-0132484P. PR 05-MAY-1999; 99US-0132485P. PR 06-MAY-1999; 99US-0132486P. PR 06-MAY-1999; 99US-0132863P. PR 07-MAY-1999; 99US-0132863P. PR 11-MAY-1999; 99US-0134256P. PR 14-MAY-1999; 99US-0134218P. PR 14-MAY-1999; 99US-013421P. PR 21-MAY-1999; 99US-0134941P. PR 20-MAY-1999; 99US-0135523P. PR 24-MAY-1999; 99US-0135529P. PR 25-MAY-1999; 99US-0136782P. PR 28-MAY-1999; 99US-0136782P. PR 28-MAY-1999; 99US-0136782P. PR 20-JUN-1999; 99US-0136782P.	25-FEB-2000; 2000EP-00; 25-FEB-1999; 99US-01; 05-MAR-1999; 99US-01; 09-MAR-1999; 99US-01; 09-MAR-1999; 99US-01; 09-MAR-1999; 99US-01; 01-APR-1999; 01-APR-199
27-AVG-1999; 99U 27-AVG-1999; 99U 31-AVG-1999; 99U 01-SEP-1999; 99U 10-SEP-1999; 99U 11-SEP-1999; 99U 13-SEP-1999; 99U 15-SEP-1999; 99U 20-SEP-1999; 99U 20-SEP-1999; 99U 22-SEP-1999; 99U 23-SEP-1999; 99U	06-AUG-1999; 99UU 06-AUG-1999; 99UU 07-AUG-1999; 99UU 10-AUG-1999; 99UU 11-AUG-1999; 99UU	PR 21-JUL-1999; 99US-0145088P. PR 22-JUL-1999; 99US-0145085P. PR 22-JUL-1999; 99US-0145089P. PR 22-JUL-1999; 99US-0145089P. PR 23-JUL-1999; 99US-0145145P. PR 23-JUL-1999; 99US-0145274P. PR 23-JUL-1999; 99US-0145274P. PR 23-JUL-1999; 99US-0145274P. PR 27-JUL-1999; 99US-0145274P. PR 27-JUL-1999; 99US-0145274P. PR 27-JUL-1999; 99US-0145218P. PR 27-JUL-1999; 99US-0145218P. PR 28-JUL-1999; 99US-0145918P. PR 28-JUL-1999; 99US-0146386P. PR 02-AUG-1999; 99US-0146388P. PR 03-AUG-1999; 99US-0146388P. PR 03-AUG-1999; 99US-014638P. PR 03-AUG-1999; 99US-0147303P. PR 04-AUG-1999; 99US-0147302P. PR 05-AUG-1999; 99US-0147302P. PR 05-AUG-1999; 99US-0147302P. PR 05-AUG-1999; 99US-0147302P. PR 05-AUG-1999; 99US-0147302P.	09-JIL-1999; 99U 12-JUL-1999; 99U 13-JUL-1999; 99U 14-JUL-1999; 99U 15-JUL-1999; 99U 16-JUL-1999; 99U 16-JUL-1999; 99U 19-JUL-1999; 99U 20-JUL-1999; 99U 20-JUL-1999; 99U

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RESULT 22
AAG33445
ID AAG33
XX AAG33
XX AAG33
XX PAG4
DT 18-OC
XX PCOLE
KW PCOLE
KW POLE
KW LETMI
XX EE M
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XX EP103
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Best Local S
Matches 12
    25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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28-SEP 1999
04-OCT 1999
06-OCT 1999
07-OCT 1999
17-OCT                                                                                                                           25-FEB-2000;
                                                                                                                                                                 06-SEP-2000.
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hybridisation
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                                                                                                                                                                                                                                                                                                                          identification; signal transduction
                                                                                                                                                                                                                                              subsp.
                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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nilarity 50.0%;
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    99US-0121825P.
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99US-0125788P.
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expression control;
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RESULT 23
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hybridisation
termination se
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sation assay; genetic mapping; gene expression control; promoter;
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99US-01342219 99US-01342219 99US-01342219 99US-01342719 99US-0134768 99US-0135339 99US-01350219 99US-013620219 99US-0137528 99US-0137528 99US-0137528 99US-0138540 99US-0139452 99US-0139452 99US-0139454 99US-0139454 99US-0139458 99US-0139458 99US-0139458 99US-0139458 99US-0139458 99US-0139458 99US-0139458 99US-0139458 99US-014958 99US-0140559 99US-0140559 99US-0140559 99US-0140559 99US-0140559 99US-014257 99US-014257 99US-014257 99US-014257 99US-014258 99US-0143318 99US-01443318	
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-call interactions in higher eukaryotes for the development of
                                                                        New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                              Venter
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                                                                                                                                                                                                                                  WO200171042-A2
                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 7953
                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                      ABB60387;
                                                                                                                                                                                                                                                                                                                                                       ABB60387 standard; protein; 1049
                                              Disclosure;
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8-OCT-1999;
9-OCT-1999;
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99US-0161406P
99US-0161359P
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99US-0161993P.
99US-0162142P.
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                                                                        detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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Pred. No. 27;
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                                             Sequence Listing;
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RESULT 25
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disord neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                             Novel 1405 isolated polypeptides, useful for diagnosis, prevention of neural, immune system, muscular, reproduct
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                                                                                                                                                                                               Claim 11; SEQ
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                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
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nonary, cardiovascular, r
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Pred. No. 92;
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myccardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, baterial, fungal and parasitic

marrow and ä

Note: The sequence data

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RESULT 26
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XX ABG15
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XW Human
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Best Local :
                                                                                                                                                                                                                                                                 sequences. (I) is useful as hybridisation proces, polymerus, reaction (PCR) primers, oligomerus, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders.
                                                                                                                                                                        involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                            patent did not appear in the printed specification, electronic format directly from WIPO at
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amino acid
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #15079
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                                                                                     to produce other types of data and products dependent on DNA and no acid sequences. ABG00010-ABG30377 represent novel human diagnostic no acid sequences of the invention. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   printed specification, but was obtained in electronic
m WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local S
Matches 8
The invention relates to human aminoacyl-tRNA synthetases (ATRS) and their corresponding nucleic acids. ATRS is useful in screening for a compound that modulates the activity of the polypeptide or that binds to the polypeptide. ATRS is also useful as an immunogen for preparing polyclonal or monoclonal antibodies by hybridoma technology. The agonist and antagonist of ATRS are useful for treating a disease or condition associated with decreased or overexpression of functional ATRS in a patient. ATRS, its DNA and its modulators are useful for diagnosis, treatment and prevention of cell proliferative disorders such as cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systemic lupus erythematosus; systemic sclerosis; ulcerative colitis; haemodialysis; uveitis; infection; single nucleotide polymorphism; gene therapy; cytostatic; dermatological; antiulcer; antibacterial; virucide; antiparastic; protozoacide; tranquilliser; vulnerary; human immunodeficiency virus; antiinflammatory; nephrotropic;
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                                                                                                                                                                                                                                                                                                                                                                              Novel human aminoacyl-tRNA synthetase polypeptides and polynucleotides for diagnosing, preventing or treating Addison's disease, allergies, asthma, rheumatoid arthritis, scleroderma, systemic lupus erythematosu
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01-JUN-2000; 2000US-0208791P.
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DB; AAD25342.
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RESULT 28
AAB43285
ID AAB43
XX AAB43
XX AAB43
XX DH Human
XX Human
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antitharenic; gene therapy; cancer; proliferative disorder; hypottension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis, autoimmune haemolytic anaemia, autoimmune thyroiditis, crohn's disease, atopic dermatitis, diabetic mellitus, Graves' disease, glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis, uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections and trauma. ATRS DNA is also useful for generating hybridisation probes useful in mapping the naturally occurring genomic sequence and oligonucleotide primers derived from it are useful to detect single nucleotide polymorphisms. ATRS DNA is used in gene therapy. The present sequence is human ATRS-3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiparkinsonian; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis and psoriasis, autoimmune/inflammatory disorders such as acquired immune deficiency syndrome (AIDS), adult respiratory distress syndrome, Addison's disease, allergies, anaemia, asthma,
Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000WO-US008621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2000.
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                                                                                                                      N-PSDB;
                                                                                                                                                      WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF3049 polypeptide sequence SEQ ID NO:6098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB43285 standard; protein; 631 AA
                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                     RA.
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                                                                                                                                                                                                                                                                                                                                                                                   2000US-00540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                 Leach
                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0127607P.
99US-0127636P.
99US-0127728P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
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                                               trame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypertension;
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RESULT 29
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antlinflammatory disease; to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be
New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM80775 standard; protein; 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 631 AA;
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anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour-associated antigenic target (TAT) polypeptide PRO81404, SEQ:1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative disorders and cardiovascular disease.
                                                              N-PSDB; ACN38464.
                                                                                                                                                                                                     02-OCT-2002; 2002US-0414971P.
                                                                                                                                                                                                                                             29-SEP-2003; 2003WO-US028547
                                                                                 WPI; 2004-347921/32.
                                                                                                                                                                                                                                                                                                                        WO2004030615-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
12; Conserv
                                                                                                                                                               GENENTECH INC
                                                                                                                     Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 5281-5283; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                         Zhou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB
Pred. No. 72;
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CC The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related nucleic acids. The TAT polypeptides are CC overexpressed in cancer tissues compared to normal tissues, and may thus CC serve as effective targets for the diagnosis and treatment of cancer in CC mammals. The invention also relates to nucleic acid and polypeptide CC sequences at least 80% identical to the TAT nucleic acids and CC polypeptides, expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic CC acid; an antibody specific for a TAT polypeptide; a peptide or organic CC molecule which binds to a TAT polypeptide; fusion proteins comprising a CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, CC diagnosis of cancer, particularly cancers such as breast cancer, CC increased TAT expression, particularly cancers such as breast cancer, CC cancer, pancreatic cancer, cervical cancer, liver cancer, bladder CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence CC represents a TAT polypeptide of the invention
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           Kable AE, Elliott VS, Tran UK, Ramkumar J, Meichardson TW, Bulloch SA, Khare R, Lee SY, Swarnakar A, Becha SD, Hafalia AJA, Chang H, Gietzen KJ, He A, Forsythe IJ, Sprague WW, I
                                                                                                                                           10-MAY-2002; 2002US-0379843P.
24-MAY-2002; 2002US-0383457P.
31-MAY-2002; 2002US-0384699P.
06-JUN-2002; 2002US-0387265P.
                                                                                                                                                                                                                                                                                                                                                                                                                       human; nucleic acid-associated protein; NAAP; autoimmune disorder; inflammatory disorder; AIDS; allergy; infection; metabolic disorder; obesity; reproductive disorder; infertility; neurological disorder; Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
                                                                                                                                                                                                                                       09-MAY-2003; 2003WO-US014450
                                                                                                                                                                                                                                                                              20-NOV-2003.
                                                                                                                                                                                                                                                                                                                WO2003094848-A2
                                                                                                                                                                                                                                                                                                                                                                                                        myocardial infarction; hypertension; eye disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI16244 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; SEQ ID NO 1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate cancer or tumor.
                                                                                                           (INCY-) INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVRCQEMGARAAKAVESGALELSPSFH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid-associated protein (NAAP) #29
                                                                                                                                                                                                                                                                                                                                                                                     disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. breast, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colorectal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
               Marquis JP, Chawla NK;
, Lal PG, Tang YT, Yue
H, Baughn MR, Borowsky
Blake JJ, Warren BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 694;
n MR, _
Warren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>
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RESULT 31
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ID ABB088919
AC ABB08
XX ABB08
XX Humar
XX Humar
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XX Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                   Region
                                                                                                                Region
                                                                                                                                                                                                                                                                                                                        Human; aminoacyl tRNA synthetase; ATRS-1; valyl-tRNA synthetase; Class I; Rossman fold; cell proliferative disorder; cancer; psoriasis; atherosclerosis; cirrhosis; hepatitis; autoimmune disorder; altergy; acquired immunodeficiency syndrome; AIDS; anaemia; diabetes; dermatomyositis; polymyositis; rheumatoid arthritis; trauma; infection; immunomodulator; immunosuppressive; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reproductive disorders (e.g. infertility), neurological disorders (e.g Parkinson's disease and Alzheimer's disease), cardiovascular disorders (e.g. myocardial infarction and hypertension), eye disorders, or cell proliferative diseases (e.g. cancer). The present amino acid sequence represents a human NAAP protein of the invention.
               Region
                                            Region
                                                                                                                                                              Region
                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                             antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human aminoacyl tRNA synthetase (ATRS-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune/inflammatory disorders (e.g. AIDS and allergies), in (e.g. bacterial and viral), metabolic disorders (e.g. obesity),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises the amino acid and coding sequences of l nucleic acid-associated proteins (NAAP). The DNA and protein set invention are useful in diagnosing, preventing and treating diseases/conditions associated with altered expression of NAAP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human nucleic acid associated proteins and polynucleotides, useful for diagnosing, preventing or treating diseases or conditions associated with aberrant protein expression, e.g. cancer, AIDS, atherosclerosis or
                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB08919 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2004-011999/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 FVRCQEMGARAAKAVESGALELSPSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADI16294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              961 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ison CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                 /note= "Aminoacyl tRNA synthetase Class I signature motif"
                                            351. .368
                                                                                                                                                                                                                                                  Location/Qualifiers
                              /note= "Valyl-tRNA
                                                                                        146. .157
                                                                                                      /note=
                                                                                                                                                                                          note= "Aminoacyl tRNA synthetase Class
                                                                                                                                                                                                                       /note= "Cytosolic N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 1063
                                                                                                                                                                                                                                       .612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; 400pp;
                                                                                                                                                                                                                                                                                                            therapy; enzyme
                                                                                                                                                              .181
                                                                                                                                                                                                       . 794
                                                                                      .150
e= "Valyl-tRNA synthetase signature motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.8%;
                .480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lindquist
 "Valyl-tRNA
                                                                         "Aminoacyl tRNA synthetase Class I signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                              synthetase
   synthetase
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signature
                            signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 961;
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Region

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RESULT 32
ADJ70652
ID ADJ70
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AC ADJ70
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DT 06-M4
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DT 06-M4
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Mitoo
KW Mitoo
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                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel human aminoacyl tRNA synthetase CC designated ATRS-1 (ABB08919) and cDNA encoding it (ABA97729). ATRS-1 is CC thought to be a valyl-tRNA synthetase, based on its 50% homology to mouse CC valyl-tRNA synthetase, based on its 50% homology to mouse CC valyl-tRNA synthetase and the presence of a tRNA synthetase Class I (I, CC L, M and V) domain. Class I enzymes such as ATRS-1 contain a catalytic CC domain based on a nucleotide-binding motif known as the Rossman fold, and CC add amino acids to the 2' hydroxyl group at the 3' end of tRNAs. ATRS-1 cC cucleotides, polypeptides, agonists and antagonists may be used for CC diagnosing, treating or preventing disorders associated with aberrant CC expression of aminoacyl tRNA synthetases. Such disorders include cell CC cirrhosis and hepatitis); autoimmune or inflammatory disorders (e.g., cancers, psoriasis, atherosclerosis, CC allergies, AIDS (acquired immunodeficiency syndrome), anaemia, diabetes, CC dermatomyositis, polymyositis and rheumatoid arthritis); trauma; and CC viral, bacterial, fungal, parasitic, protozoal or helminthic infections. They are also useful in screening for modulators of ATRS-1 expression or artivity. The present sequence represents human aminoacyl tRNA synthetase
                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                      Sequence 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New aminoacyl tRNA synthetases, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergies or anemia) or cell proliferative disorders (e.g. cancers, atherosclerosis o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 89-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-599795/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-2000; 2000US-0255963P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2001; 2001WO-US048575
                                                 Human heat mitochondrial protein as a therapeutic target SeqID2458.
                                                                                                                                               ADJ70652 standard; protein; 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatitis).
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                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                     1 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baughn MR;
                                                                                                                                                                                                                                  FVRCQEMGARAAKAVESGALELSPSFH 507
                                                                                                                                                                                                                                                                   YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= Transmembrane_domain
                                                                                  entry)
                                                                                                                                                                                                                                                                                                                   36.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .634
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                                                                                                                                                                                                                                                                                                 Score 50; DB 5;
Pred. No. 1.3e+02;
4; Mismatches 11
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ADK40961
ID ADK40
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AC ADK40
XX O6-MA
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XX Novel
XX cytos
KW antig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
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17-JUN-2002; 2002US-0389987P
20-SEP-2002; 2002US-0412418P
                                                                                                                       Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating the state of the sample and correlating the sample and cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ghosh SS,
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                                                                                                                                                                                   06-MAY-2004
                                                                                                                                                                                                                                                                                                    ADK40961 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to novel mitochondrial targets that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-845369/78
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12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVRCQEMGARAAKAVESGALELSPSFH 507
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                                                                                                                    kinase protein #68
                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA,
                                                                                                                                                                                                                                                                                                 protein; 1078 AA.
                                                                                                                                                                                entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 7; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1063;
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cytostatic; immunomodulator; cardiant; neuroprotective; nootropic; antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological; analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase;

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RESULT 34
ADR15680
ID ADR15
XX
AC ADR15
XX
DT 04-NC
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                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                      cc molecules encoding a kinase polypeptide. The nucleic acid molecules comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a c complement of (a); (c) hybridizes under stringent conditions to (a) and c complement of (a); (c) hybridizes under stringent conditions to (a) and c complement of (a); except that it lacks one or more, but not all, of an collegation of the control of the conditions to an except that it lacks one or more, but not all, of an c c c terminal domain, a coiled-coil structure region, a spacer region and a c-c terminal tail; or (e) is a complement of (d). The nucleic acid molecules, c polypeptides, methods and substance are useful for treating cancers, c meuronal-associated diseases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, disease, c the central or peripheral nervous system, Alzheimer's disease, c c c the central or peripheral nervous system, Alzheimer's disease, c c c viral infections, infections caused by prions, infections caused by fungi, ocular diseases, migraines, pain, c sexual dysfunction, mood disorders, accular diseases, cognition of isorders, cognition.
                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; peripheral nervous system; central nervous system; Alzheimer; disease; Parkinson; disease; multiple sclerosis; amyotrophic lateral sclerosis; viral infection; prion infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; neurological disorder; dyskinesia; metabolic disorder; organ transplant rejection; enzyme.
    04-NOV-2004
                                                                              ADR15680 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovasculated disease, brain or neuronal-associated diseases and
                                          ADR15680;
                                                                                                                                                                                                                                                                                                                                    Sequence 1078 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 68; 491pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-DEC-2001; 2001US-0343169P
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                                                                                                                                                                                                                                                        12;
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SUDARSANAM S.
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                 FVRCQEMGARAAKAVESGALELSPSFH 495
                                                                                                                                                                                                               YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders.
                                                                                                                                                                                                                                                                                                                                                                                     hypotension, hypertension, psychotic disorders, neurological dyskinesias, metabolic disorders and organ transplant This sequence corresponds to one of the kinase polypeptides of
                                                                                                                                                                                                                                                        Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sudarsanam
                                                                            protein; 1078 AA.
                                                                                                                                                                                                                                                                        36.8%;
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                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                        Score 50; DB 7;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                          Length 1078;
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                                                                                                                                                                                                                                                      Gaps
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ABP66271
ID ABP
XX
AC ABP

ABP66271 standard; protein; 187

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                                                                                                                                                                                                                                                                      cc embedded into the secondary structure pattern (CRISSP), which are used to condered the condered to the referent protein family, wherein said condered to the referent protein family, wherein said condered to illustrate the method of the invention. The gequence is a kinase, used to illustrate the method of the invention. The chinases are useful for diagnosing or treating various kinase-related concers, and disorders, cardiovascular disease, brain or neuronal concert diseases and disorders, cardiovascular disease, brain or neuronal concert are cancers of tissues, cancers of the peripheral concert are cancers of tissues, cancers of the peripheral concert are cancers of tissues, cancers of the peripheral concert are cancers of diseases of the central nervous system, diseases of the peripheral concert and the cancer of the peripheral concert and the cancer of the peripheral concert and the control scales of the peripheral concert and the control of the peripheral concert and the control of the peripheral concert and the 
                                                                                                                             Query Match
Best Local :
                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for detecting remote polypeptide homologues, comprising analysis of conserved secondary structure pattern in a protein family, and conserved active site an acid residues. The analyses are used to identify conserved residues
                                                                                                                                                                                                        Sequence 1078 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated, enriched, or purified kinase nucleic acids and polypeptides, useful for diagnosing or treating kinase-related diseases and conditions, e.g. cardiovascular disease, brain or neuronal-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADR15757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunosuppressive; Gene Therapy; kinase; enzyme; cancer; immune-related disease; cardiovascular disease; neuronal-associated disease; metabolic disorder.
                                                                                                                                                                                                                                                           dyskinesias, metabolic disorders, or organ transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Fig 2; 496pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-604329/58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; Cardiovascular; Neuroprotective; Nootropic; Antipar Virucide; Cerebroprotective; Antibacterial; Fungicide; Ophthalm Virucide; Analgesic; Endocrine; Tranquillizer; Hypotensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-2003; 2003WO-US002234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GRIG/) GRIGORIEV I V.
(SUDA/) SUDARSANAM S.
                                                N
                                                                                                  . Similarity 12; Conserv
FVRCQEMGARAAKAVESGALELSPSFH
                                                  YVFSTEMANKAAEAVLKGQVETIVSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or metabolic disorders.
                                                                                                     Conservative
                                                                                                                             36.8%;
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                                                                                                  4
                                                                                                                           Score 50;
Pred. No.
                                                                                                     Mismatches
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495
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                                                                                                                                1.4e+02;
                                                                                                                                                     DB 8;
                                                                                                                                                   Length 1078
                                                                                                     Indels
                                                                                                                                                                                                                                                           rejection
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Ophthalmological;
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AC ABO6
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                                                                                                                                                                                                                                                                                                                        CC heterologous polypeptide. (I) has antidiarrheic and antibacterial CC activities, and can be used as an inhibitor of Salmonella. (I) (which is CC a probe) is useful for the detection and/or identification of CC Bifidobacterium longum in a biological sample. A carrier containing the CC lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be CC used for preventing and/or treating diarrhoea brought about by pathogenic CC bacteria and/or rotavirus. The carrier is a food composition selected CC products, cice-creams, fermented cereal based products, milk based fermented CC products, ice-creams, fermented cereal based products, milk based CC powders, infant formula, pet food or a pharmaceutical composition CC selected from tablets, liquid bacterial suspensions, dried oral CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or Chips to carry out analysis of the CC expression of the Bifidobacterium gene. ABG81844 to ABG81850 represent CC Listing from the present invention but not mentioned further within the Sequence data for this patent is not represented CC in the printed specification but is based on sequence information CC supplied by the European Patent Office
                                                                               RESULT 36
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at least 90% identity or which hybridises with the sequences given in ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding fusion protein, comprising a sequence selected from 1097 sequences given in ABP65258 to ABP6354 ligated in frame to a polynucleotide encoding a heterologous polyneride (II) has apridication and applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection;
    ABO61084;
                                                                                                                                                                                                                                                                                           Sequence 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; SEQ ID NO 1015; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-668397/72.
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                                        ABO61084 standard; protein; 265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001EP-00102050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rotavirus; food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:1015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide comprising
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                                                                                                                                       EMAALASEDYRDKNPLLVAVLKGAVNTLVAF 56
                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                   36.0%;
                                                                                                                                                          -AVLKGQVETIVSF 27
                                                                                                                                                                                                            Score 49; DB
Pred. No. 24;
3; Mismatches
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                                                                                                                                                                                                                                                     Length 187;
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Matches
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 21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a new isolated nucleic acid encoding a Klebsiel pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a
                                                                                                                                                                                                        19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #35203.
                                                                                                                                                                                                                                                        ABU49676 standard; protein; 586
                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 7601; 932pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae polypeptide seqid 7601
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                                                            21-MAR-2002;
                                                                                   03-OCT-2002.
                                                                                                          WO200277183-A2
                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design
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                                                                                                                                                                                                                                                                                                                                                                   h 36.0%;
Similarity 45.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   265 AA;
                                                                                                                                                                                                                                                                                                                    MANRAPYAIMKSAVETLTRY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osborne
2001US-00815242.
2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                                            2002WO-US009107
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                                                                                                                                                                                                                                                                                                                                                                              Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         Length 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a Klebsiella
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ABJ25889
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AC ABJ7
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EW Fung
KW Fung
KW Cand
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Best Local
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Aspergillus fumigatus
                                                    cancer; contamination;
                                                                          Fungicide; cytostatic;
                                                                                                                           Aspergillus fumigatus essential gene protein #547.
                                                                                                                                                                                                                                          ABJ25889;
                                                                                                                                                                                                                                                                                        ABJ25889 standard; protein; 984 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 586
                                                                                                                                                                                     16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-029926/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are the nucleic acid a vector comprising a promoter operably linked to the nucleic acid a vector comprising a promoter operably linked to the nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                       YIFYSQVMTKAPLLLGLVTLIGYWLLRRDATTIIKGSIKTIVGF 52
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA,
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.0%;
                                              essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB
Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for rational drug discovery programs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
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Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Xu HH;
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RESULT 39
ABJ26489
ID ABJ26
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AC ABJ26
AX
DT 16-AE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a
                    Aspergillus
                                                           16-APR-2003
                                                                                                  ABJ26489
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       factors. This sequence represents a protein of of Aspergillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295890P.
09-UUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                     ABJ26489 standard; protein; 1058 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200286090-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002; 2002WO-US013142
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                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                          500
                                                                                                                                                                                                                                                                           3 VFSTEMANKAAEAVLKGQV 21
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                984 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tishkoff D,
                    fumigatus essential
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                      36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zamudio C,
                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                      Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eroshkin AM, Hu W,
                                                                                                                                                                                                                                                                                                                                      1.8e+02;
                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                         Length 984;
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gene protein #1147

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RESULT 40
ADC50023
ID ADC50
XX
AC ADC50
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                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel purified or isolated nucleic acids of CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic corganism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a comprising A. fumigatus. The polynucleotides are useful for characterisation, screening or corganisms invade or reside, for comparing with the DNA sequence of A. CC fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify optential orthologous essential or virulence genes, for selecting and comparing of comparing or comparing with DNA sequences of other related or distant pathogenic organisms to identify on antipodice or antipodice, as an antipodice or identify on antipodice or comparing with DNA comparing of other related or distant pathogenic organisms to identify on antipodice or identify on antipodice or comparing with DNA comparing of or antipodice or comparing with DNA comparing of openical antipodices, as an antipodice or antipodice, and to identify inhibitors of the binding course or to identify inhibitors of the binding course or to identify inhibitors of the binding course of the protein in biological fluids, as a marker for comparing with pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence corganism invade or reside, and to isolate correlative receptors or ligands in the case or virulence corganism invade or reside, and to isolate organism such antipodice of the essential genes of happergillus fumigatus of the invention
                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
cancer; contamination; biofilm; antibody; immune response.
                     ADC50023
                                                                                                                                                                                                                                                                                                                               Sequence 1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-093124/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002; 2002WO-US013142
                                                          ADC50023 standard; protein; 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus fumigatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-)
                                                                                                                                                                                                                                                                 Local
                                                                                                                                                               500
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                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                               VYRANMANKSAAAVLKSKL 518
                                                                                                                                                                                                    VFSTEMANKAAEAVLKGQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC.
                                                                                                                                                                                                                                                                 36.0%;
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                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                             Score 49; DB 6;
Pred. No. 1.9e+02;
4; Mismatches 5
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                                                                                                                                                                                                                                                                                    Length 1058;
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                                                                                                                                                                                                                                           Gaps
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Best Local S
Matches 11
                                                                                                                                                                     The invention relates to gene repair function associated protein-34.1 (ADC50023) and nucleic acids encoding it (ADC50022). The protein has a molecular weight of 34.1 kD, and has 34% identity and 47% homology over 235 amino acid stretch with an Arabidopsis thaliana DNA repair protein-like protein (GenBank accession number AB016875). The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications. Gene repair function associated protein-34.1 can be used in the treatment of a variety of diseases such as cancer, blood diseases, HIV (human immunodeficiency virus) infection and immune disorders. The present sequence represents gene repair
                                                                                                                                                                                                                                                                                                                                                                                      New gene repair function associated protein-34.1, encodi polynucleotide, antagonist, and recombinant production, treating cancer, hemopathy, HIV and immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene repair function associated protein-34.1; macroprotein-51.59; recombinant production; gene therapy; tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; cytostatic;
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADC50022.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2; 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN1382717-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunomodulator.
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                                                                                Similarity
                                                                                                                                310
YVFTSEKANQEEDIPVKGSHSTKVEAVV
                                    YVFSTEMANKAAEAVLKG----QVETIV 25
                                                                                                                                                             associated protein-34.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function
                                                                    Conservative
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                                                                                35.3%;
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                                                                  Score 48; DB Pred. No. 64; 7; Mismatches
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         143
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                                                                                                Length 310,
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